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rotein - protein search, using sw model

n: January 6, 2004, 11:20:38 ; Search time 22 Seconds  
(without alignments)  
898.144 Million cell updates/sec

US-10-038-517-2

ct score: 2527

nce: 1 MGIIWVAFLEFGTSRGKEV.....STFCSDIMGNILQNLKPC 467

ng table: BLOSUM62

Gapop 10.0 , Gapext 0.5

hed: 328717 seqs, 42310858 residues

number of hits satisfying chosen parameters: 328717

um DB seq length: 0

um DB seq length: 2000000000

Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

ase : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A.COMB.pap:\*
- 2: /cgn2\_6/ptodata/2/iaa/5B.COMB.pap:\*
- 3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pap:\*
- 4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pap:\*
- 5: /cgn2\_6/ptodata/2/iaa/PTCUS.COMB.pap:\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID	Score	Query Match	Length	DB	Description
1	2523	99.8	467	4	US-09-411-132A-3
2	1180	46.7	473	4	US-09-411-132A-7
3	1174	46.5	467	4	US-09-411-132A-9
4	1172	46.4	473	4	US-09-411-132A-8
5	1166	46.1	467	4	US-09-411-132A-10
6	1162	46.0	467	4	US-09-411-132A-4
7	1152	45.6	469	4	US-09-411-132A-5
8	1152	45.6	469	4	US-09-411-132A-5
9	1115	44.1	465	4	US-08-985-432-15
10	534	21.1	499	4	US-09-411-132A-6
11	515.5	20.4	500	4	US-08-985-432-8
12	462.5	18.3	345	4	US-08-985-432-10
13	462.5	18.3	353	4	US-08-985-432-4
14	462.5	18.3	354	4	US-08-985-432-6
15	440.5	17.4	472	4	US-08-985-432-13
16	391.5	15.5	124	1	US-08-180-209B-21
17	391.5	15.5	124	1	US-08-385-745-21
18	391.5	15.5	124	3	US-08-485-388-21
19	391.5	15.5	124	3	US-08-474-853-21
20	391.5	15.5	124	4	US-08-166-205B-21
21	391.5	15.5	124	5	PCT-US94-02629-21
22	307	12.1	125	1	US-08-180-209B-20
23	307	12.1	125	1	US-08-745-20
24	307	12.1	125	3	US-08-485-388-20
25	307	12.1	125	3	US-08-474-853-20
26	307	12.1	125	4	US-09-166-205B-20
27	307	12.1	125	5	PCT-US94-02629-20

Sequence 64, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 19, Appl  
Sequence 18, Appl  
Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-411-132A-3  
Sequence 3 Application US/09411132A  
Patent No. 6558936  
GENERAL INFORMATION:  
APPLICANT: Khodadoust, Mehran  
APPLICANT: Kapeller-Libermann, Rosana  
TITLE OF INVENTION: No. 6558936 Human Lipase Proteins, Nucleic Acides Encoding  
TITLE OF INVENTION: Them, and Uses of Both of These  
FILE REFERENCE: 10147-14  
CURRENT APPLICATION NUMBER: US/09/411.132A  
CURRENT FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-411-132A-3

Query Match	99.8%	Score 2523	DB 4	Length 467
Best Local Similarity	99.8%	Pred. No. 1.6e-262		
Matches 466	Conservative 1	Mismatches 0	Indels 0	Gaps 0
QY	1	MLGIWVAFLEFGTSRGKEVCYERLGC	1	MLGIWVAFLEFGTSRGKEVCYERLGC
DB	1	MLGIWVAFLEFGTSRGKEVCYERLGC	1	MLGIWVAFLEFGTSRGKEVCYERLGC
QY	61	IHNPNAYOEISAVNSSTIOASYFGTDK	61	IHNPNAYOEISAVNSSTIOASYFGTDK
DB	61	IHNPNAYOEISAVNSSTIOASYFGTDK	61	IHNPNAYOEISAVNSSTIOASYFGTDK
QY	121	LDWINGSREYTHAVNNLRVGAEVAF	121	LDWINGSREYTHAVNNLRVGAEVAF
DB	121	LDWINGSREYTHAVNNLRVGAEVAF	121	LDWINGSREYTHAVNNLRVGAEVAF
QY	181	IPGLGRITGLDPAAGFFHNTPKVRLD	181	IPGLGRITGLDPAAGFFHNTPKVRLD
DB	181	IPGLGRITGLDPAAGFFHNTPKVRLD	181	IPGLGRITGLDPAAGFFHNTPKVRLD
QY	241	FYPNGGKMPCEDLITPLKFNFNAYK	241	FYPNGGKMPCEDLITPLKFNFNAYK
DB	241	FYPNGGKMPCEDLITPLKFNFNAYK	241	FYPNGGKMPCEDLITPLKFNFNAYK
QY	301	CRSYTSFKAGNCFCSKEGCGTNGHFA	301	CRSYTSFKAGNCFCSKEGCGTNGHFA
DB	301	CRSYTSFKAGNCFCSKEGCGTNGHFA	301	CRSYTSFKAGNCFCSKEGCGTNGHFA
QY	361	VKLSSSVTQGVFLRVGAIGTKGFAI	361	VKLSSSVTQGVFLRVGAIGTKGFAI
DB	361	VKLSSSVTQGVFLRVGAIGTKGFAI	361	VKLSSSVTQGVFLRVGAIGTKGFAI

3 - see 20 No 3

361 VKLSGSEVTOGTFLRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDAEVAVGNITSVQFTW 420  
421 KKHLPDSQKLGAEWINTSGKYGYKSTFCSDIMGNILQNLKPC 467  
421 KKHLPDSQKLGAEWINTSGKYGYKSTFCSDIMGNILQNLKPC 467

AT 2  
US-411-132A-7  
Sequence 7, Application US/09411132A  
Patent No. 6558936  
GENERAL INFORMATION:  
APPLICANT: Khodadoust, Mehran  
PLICANT: Kapeller-Libermann, Rosana  
TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding  
TITLE OF INVENTION: Them, and Uses of Both of These  
FILE REFERENCE: 10147-14  
CURRENT APPLICATION NUMBER: US/09/411,132A  
CURRENT FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 7  
LENGTH: 473  
TYPE: PRT  
ORGANISM: Mus musculus  
US-411-132A-7

Query Match 46.7%; Score 1180; DB 4; Length 473;  
Best Local Similarity 49.0%; Pred. No. 5.4e-118;  
Matches 231; Conservative 73; Mismatches 159; Indels 8; Gaps 6;  
QY 1 MLCIWIIVAFVFGTSGRGKVCYERLGCFCFQDGLPWTFTSTELVGLPWSPEKINTRELLYT 60  
DB 1 MLCIWIIVAFVFGTSGRGKVCYERLGCFCFQDGLPWTFTSTELVGLPWSPEKINTRELLYT 60  
QY 61 IHNPNAYQEI SAVNSSTIQASYFGTDKITRINIAGW--KTDGKWQDMCNVLLQLEDINC 118  
DB 61 IHNPNAYQEI SAVNSSTIQASYFGTDKITRINIAGW--KTDGKWQDMCNVLLQLEDINC 120  
QY 119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKFYSKVKHLIGHSLGAHLAGEA 177  
DB 121 ICVDWKKGSTQTTQAAANNRVVGAQVQMLDILVRNFYSASKVKHLIGHSLGAHVAGEA 180  
QY 178 GSRIPLGLGRITGLDPAGPFFHNTPKVEVLDPDANFVDVHTNAARILFELGVGTIDACG 237  
DB 181 GSRTPLGLGRITGLDPVEANFEGTPEEVLDPDADFVDVHTDAAPLIPFLGFTSQMG 240  
QY 238 HLDYPNGGKHMFGC-EDLITPLKFNFNAYKKEWASFFDCNHARSYQFYAESILNPDFA 296  
DB 241 HFDFFPNGGQYMPGCKKNALSQIV--DIDGIWSGTRDFVACNHLRSYKYLESILNPDGF 298  
QY 297 IAYPCRSYTSFKAGNCFKSCGECPTMGHFAFRHFKMKNTGSHYFLNTGSLSPFARWR 356  
DB 299 AAYPCASYRPFESNKCFCPCDQCPQMGHYADKFAVKT-SDETQYFLNTGDSNPFARWR 357  
QY 357 HKLSVKLSGSEVTOGTFLRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVAVGNITSV 416  
DB 358 YRVSLTFSGTFTV-GQVKVSLFGSNGTRQCDIFRGIKPGATHSNEFDKLDVGTIEKV 416  
QY 417 QETWKHHLFEDSQNLGAEWINTSGKYGYKSTFCSDIMGNILQNLKPC 467  
DB 417 KFLNNHVNVPSPFKVGAAKITVQKGEERTENHFCSEETVREDILLTLTPC 467

AT 3  
US-411-132A-9  
Sequence 9, Application US/09411132A  
Patent No. 6558936  
GENERAL INFORMATION:  
APPLICANT: Khodadoust, Mehran  
PLICANT: Kapeller-Libermann, Rosana  
TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding  
TITLE OF INVENTION: Them, and Uses of Both of These

FILE REFERENCE: 10147-14  
CURRENT APPLICATION NUMBER: US/09/411,132A  
CURRENT FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 9  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-411-132A-9

Query Match 46.5%; Score 1174; DB 4; Length 467;  
Best Local Similarity 48.2%; Pred. No. 2.3e-117;  
Matches 227; Conservative 78; Mismatches 158; Indels 8; Gaps 6;  
QY 1 MLCIWIIVAFVFGTSGRGKVCYERLGCFCFQDGLPWTFTSTELVGLPWSPEKINTRELLYT 60  
DB 1 MLCIWIIVAFVFGTSGRGKVCYERLGCFCFQDGLPWTFTSTELVGLPWSPEKINTRELLYT 60  
QY 61 IHNPNAYQEI SAVNSSTIQASYFGTDKITRINIAGW--KTDGKWQDMCNVLLQLEDINC 118  
DB 61 IHNPNAYQEI SAVNSSTIQASYFGTDKITRINIAGW--KTDGKWQDMCNVLLQLEDINC 120  
QY 119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKFYSKVKHLIGHSLGAHLAGEA 177  
DB 121 ICVDWKKGSTQTTQAAANNRVVGAQVQMLDILVRNFYSASKVKHLIGHSLGAHVAGEA 180  
QY 178 GSRIPLGLGRITGLDPAGPFFHNTPKVEVLDPDANFVDVHTNAARILFELGVGTIDACG 237  
DB 181 GSRTPLGLGRITGLDPVEANFEGTPEEVLDPDADFVDVHTDAAPLIPFLGFTSQMG 240  
QY 238 HLDYPNGGKHMFGC-EDLITPLKFNFNAYKKEWASFFDCNHARSYQFYAESILNPDFA 296  
DB 241 HLDFFPNGGQYMPGCKKNALSQIV--DIDGIWSGTRDFVACNHLRSYKYSESILNPDGF 298  
QY 297 IAYPCRSYTSFKAGNCFKSCGECPTMGHFAFRHFKMKNTGSHYFLNTGSLSPFARWR 356  
DB 299 AAYPCASYRPFESNKCFCPCDQCPQMGHYADKFAVKT-SDETQYFLNTGDSNPFARWR 357  
QY 357 HKLSVKLSGSEVTOGTFLRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVAVGNITSV 416  
DB 358 YGVSLTSGKAT-QQAKVALFGSKGNTHQNFIFKILKPGSTHSNEFDKLDVGTIEKV 416  
QY 417 QETWKHHLFEDSQNLGAEWINTSGKYGYKSTFCSDIMGNILQNLKPC 467  
DB 417 KFLNNHVNVPSPFKVGAAKITVQKGEERTVHVSFSESTVREDVLLTLTPC 467

RESULT 4  
US-09-411-132A-8  
Sequence 8, Application US/09411132A  
Patent No. 6558936  
GENERAL INFORMATION:  
APPLICANT: Khodadoust, Mehran  
PLICANT: Kapeller-Libermann, Rosana  
TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding  
TITLE OF INVENTION: Them, and Uses of Both of These  
FILE REFERENCE: 10147-14  
CURRENT APPLICATION NUMBER: US/09/411,132A  
CURRENT FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 8  
LENGTH: 473  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-411-132A-8

Query Match 46.4%; Score 1172; DB 4; Length 473;  
Best Local Similarity 49.3%; Pred. No. 3.9e-117;  
Matches 232; Conservative 73; Mismatches 158; Indels 8; Gaps 6;  
QY 1 MLCIWIIVAFVFGTSGRGKVCYERLGCFCFQDGLPWTFTSTELVGLPWSPEKINTRELLYT 60

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1 MLTLVSLFLGAAQGEVYDNLGCFSDAEPWAGTAIRPLKLLPSPKINTRFLLYT 60
61 IHNPNAYOEISAVNSSTIQASVFGTDKTRINIAGW--KTDGKWORDMKNVLLQLEDINC 118
61 NENPTAFQTLQLSDPLLTIGASNFQVARKTRFIHGFIDKGEENVVDMCKMFMQVEVNC 120
119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177
121 ICVDWKKGSQITTYQOANNVRVVGAAQVADMIDILVKNYSYSPSKVHLIGHSLGAHVAGEA 180
178 GSRIPGLGRITGLDPAGFPFHTPKVELRDPDSANFVDVHTNAARILFELGVGTIDACG 237
181 GSRTPGLGRITGLDPVEANFGTETEEVRLDSDADFVDVHTDAAPLIPFLGFTNQMSG 240
238 HLDFFPNGGKHPGC-EDLITPLKKNFNAYKEMASFFDCNHSYQFYAESILNPDAF 296
241 HLDFFPNGGQMPGCKKNALSQIV--DIDGWSGTRDFVACNHLRSYKYLESILNPDPGF 298
297 IAYPCRSYTSKAGNCFKSCGECPTMGHFAHDFHFKNMKTNGSHYFLNTGSLSPFARWR 356
299 AAYPCASYKDFESNCKFCPPDQCGCPQMGHAYADKFAKS-GDEPKQFLNTGEAKNFARWR 357
357 HKLSVKLSGSEVTOGTVELRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVNGNITSV 416
358 YVSVILLSGRWVT-GQVKVALFGSKGNTQVDIFRGLIKPGATHSSEFADKLDVGTIEKV 416
417 QFIWKKHLPESQNKLGAEWVINTSGKYGYKSTFCSDQIMGNPILQNLKPC 467
417 KFLMNNQVINFSPFRVGAAKITVQKGEERTYCNFCSSETVREDTLLTLTPC 467

5
-411-132A-10
ence 10, Application US/09411132A
nt No. 6558936
RAL INFORMATION:
LICANT: Khodadoust, Mehran
LICANT: Kapeller-Libermann, Rosana
LE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding
LE OF INVENTION: Them, and Uses of Both of These
LE REFERENCE: 10147-14
RENT APPLICATION NUMBER: US/09/411,132A
RENT FILING DATE: 2000-09-12
BER OF SEQ ID NOS: 10
TWARE: PatentIn Ver. 2.1
ID NO 10
NGTH: 467
PE: PRT
GANISM: Canis familiaris
-411-132A-10

7 Match 46.1%; Score 1166; DB 4; Length 467;
Local Similarity 48.0%; Pred. No. 1.7e-116;
Matches 226; Conservative 79; Mismatches 158; Indels 8; Gaps 6;

1 MLGIWIVAFPLFGTSRKEVCYERLGCGLPWTRFTSTELVGLPWSPEKINTRFLLYT 60
1 MVSINTIALFLGAAKAKEVCYEOIGCFSDAEPWAGTAIRPLKVLPSPERIGTRFLLYT 60
61 IHNPNAYOEISAVNSSTIQASVFGTDKTRINIAGW--KTDGKWORDMKNVLLQLEDINC 118
61 NKNPNFOTLLPSPDSTIEASNFQDKKTRFIHGFIDKGEENWLLDMCKMFKVEVNC 120
119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177
121 ICVDWKKGSQITTYQOANNVRVVGAAQVADMIDILVKNYSYSPSKVHLIGHSLGAHVAGEA 180
178 GSRIPGLGRITGLDPAGFPFHTPKVELRDPDSANFVDVHTNAARILFELGVGTIDACG 237
181 GSRTPGLGRITGLDPVEASFGTETEEVRLDSDADFVDVHTDAAPLIPFLGFTSQQMG 240
238 HLDFFPNGGKHPGC-EDLITPLKKNFNAYKEMASFFDCNHSYQFYAESILNPDAF 296
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Db 241 HLDFFPNGGEMPGCKKNALSQIV--DLDCIWEGTRDFVACNHLRSYKYYESILNPDPGF 298
Qy 297 IAYPCRSYTSKAGNCFKSCGECPTMGHFAHDFHFKNMKTNGSHYFLNTGSLSPFARWR 356
Db 299 ASYPCASYRAFESNCKFCPPDQCGCPQMGHAYADKFAVKT-SDETQKIFLNTGSSNFARWR 357
Qy 357 HKLSVKLSGSEVTOGTVELRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVNGNITSV 416
Db 358 YVSVITLISGRAT-GQAKVALFGSKGNTQVDIFRGLIKPGSTHSEFADKLDVGTIEKV 416
Qy 417 QFIWKKHLPESQNKLGAEWVINTSGKYGYKSTFCSDQIMGNPILQNLKPC 467
Db 417 KFLMNNVNVNPTFPKVGAAKITVQKGEERTVHSCSESTVREDVLLTLTPC 467

RESULT 6
US-09-411-132A-4
; Sequence 4, Application US/09411132A
; Patent No. 6558936
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding
; TITLE OF INVENTION: Them, and Uses of Both of These
; FILE REFERENCE: 10147-14
; CURRENT APPLICATION NUMBER: US/09/411,132A
; CURRENT FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-132A-4

Query Match 46.0%; Score 1162; DB 4; Length 467;
Best Local Similarity 48.6%; Pred. No. 4.6e-116;
Matches 229; Conservative 75; Mismatches 159; Indels 8; Gaps 6;

Qy 1 MLGIWIVAFPLFGTSRKEVCYERLGCGLPWTRFTSTELVGLPWSPEKINTRFLLYT 60
Db 1 MLIPFTITLFLGAAKAKEVCYEDLGCFSDETPWGGTAIRPLKILPWSPEKIGTRFLLYT 60
Qy 61 IHNPNAYOEISAVNSSTIQASVFGTDKTRINIAGW--KTDGKWORDMKNVLLQLEDINC 118
Db 61 NKNPNFOTLLPSPDSTIEASNFQDKKTRFIHGFIDKGEENWLLDMCKLFEVEVNC 120
Qy 119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177
Db 121 ICVDWKKGSQITTYQOANNVRVVGAAQVADMIDILVKNYSYSPSKVHLIGHSLGAHVAGEA 180
Qy 178 GSRIPGLGRITGLDPAGFPFHTPKVELRDPDSANFVDVHTNAARILFELGVGTIDACG 237
Db 181 GSKTPGLGRITGLDPVEASFGTETEEVRLDSDADFVDVHTDAAPLIPFLGFTNQQMG 240
Qy 238 HLDFFPNGGKHPGC-EDLITPLKKNFNAYKEMASFFDCNHSYQFYAESILNPDAF 296
Db 241 HLDFFPNGGSMGCKKNALSQIV--DLDCIWAGTRDFVACNHLRSYKYLESILNPDPGF 298
Qy 297 IAYPCRSYTSKAGNCFKSCGECPTMGHFAHDFHFKNMKTNGSHYFLNTGSLSPFARWR 356
Db 299 AAYPCASYKDFESNCKFCPPDQCGCPQMGHAYADKFAKTSEEQ-QKFFLNTGEASNFARWR 357
Qy 357 HKLSVKLSGSEVTOGTVELRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVNGNITSV 416
Db 358 YVSVITLISGRAT-GQIKVALFGNKNTHQYSLFRGILKPGSTHSEFADKLDVGTIEKV 416
Qy 417 QFIWKKHLPESQNKLGAEWVINTSGKYGYKSTFCSDQIMGNPILQNLKPC 467
Db 417 KFLMNNVNVNPTLPKVGATKITVQKGEERTVYNFCSSETVREDTLLTLTPC 467
```

10-411-132A-5  
 nence 5, Application US/09411132A  
 ent No. 6558936  
 ERAL INFORMATION:  
 PLICANT: Khodadoust, Mehran  
 PLICANT: Kapeller-Libermann, Rosana  
 TLE OF INVENTION: NO. 6558936el Human Lipase Proteins, Nucleic Acides Encoding  
 TLE OF INVENTION: Them, and Uses of Both of These  
 LE REFERENCE: 10147-14  
 RRENT APPLICATION NUMBER: US/09/411,132A  
 RRENT FILING DATE: 2000-09-12  
 MBER OF SEQ ID NOS: 10  
 FTWARE: Patentin Ver. 2.1  
 ID NO 5  
 LENGTH: 469  
 YPE: PRT  
 RGANISM: Homo sapiens  
 -411-132A-5  
 ry Match 45.8%; Score 1152; DB 4; Length 469;  
 t Local Similarity 47.8%; Pred. No. 5.5e-115;  
 ches 225; Conservative 68; Mismatches 172; Indels 6; Gaps 5;  
 1 MLGIWIVARLFFGTSRGKVCYERLGCPCDGLPWTSTELVGLPWSPEKINTREFLLYT 60  
 1 MLPFWLGLLLATVAGKEVCYQLGCFSDERPWAGTLQRPVKLLPWSPEIDIDREFLLYT 60  
 61 IHNPNAYQEISAVNSSTIOASYFGTDKITRINIAGW--KTDGKWORDMNCVLLQLEDINC 118  
 61 NENPNFQILITGTEPDITBASNPQLDRKTRFIHGFIDKAEDESPDMCKMFEVKVNC 120  
 119 INLDWINGSRE-YIHAVNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGSLGAHLAGEA 177  
 121 ICVDWHRGSRAMYTQAVQIRVVGAETFLIOALSTQLGYSLEDVHVHIGSLGARTAAEA 180  
 178 GSRIPG-LGRITGLDPAGFPFHNTPREVRLDPSDANFVDVIHTNAARILFELGVGTIDAC 236  
 181 GRLGRVGRITGLDPAGFCODEPEVEVRLDPSDAVFDVVIHTDSSPIVPSLGFMSQKV 240  
 237 GHLDFFPNGKHEMPCGEDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESILNPDAF 296  
 241 GHLDFFPNGKHEMPCGCKNVLSTIT-DIDGIWEGIGGFVSCNHLRSFEYSSVNLNPDGF 299  
 297 IAYPCRSYTSFKAGNCFKCEGCPMTGHFADRFHFKMKTNGSHYFLNTGSLSPFARWR 356  
 300 LGYPCASYDEFQESKCFPCPAEGCPKMGHYAQPKGKTSABEQT-FFLNTGESGNFTSWR 358  
 357 HKLSVKLSGSEVTOGTVFLRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVNGNITSV 416  
 359 YKVSVTLSGKEKNGYIRIALYGSNENSKQYBIFKGLPKPDASH\*CAIDVDVFNVGKIQV 418  
 417 QFTWKXHLFPEDSQNKLAGEMVINTSGKYKSTFCSDQIMGNILQNLKPC 467  
 419 KFLWNRGINLSPKLGASQITVQSGEDGTEYFNFCSSDTVEENVLQSLYPC 469  
 10-985-492-15  
 nence 15, Application US/08985492  
 ent No. 6195530  
 ERAL INFORMATION:  
 APPLICANT: Jaye, Michael C.  
 APPLICANT: Doan, Kim-Anh T.  
 APPLICANT: Krawiec, John A.  
 APPLICANT: Lutch, Kevin J.  
 APPLICANT: Amin, Dilip V.  
 APPLICANT: South, Victoria J.  
 TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
 TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
 TITLE OF INVENTION: IN ENZYMIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 STREET: 500 Arcola Rd. 3C43  
 CITY: Collegeville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,492  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fehlner Ph.D., Paul F.  
 REGISTRATION NUMBER: 35,135  
 REFERENCE/DOCKET NUMBER: A2582-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610)454-3839  
 TELEFAX: (610)454-3808  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 465 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-985-492-15  
 Query Match 44.1%; Score 1115; DB 4; Length 465;  
 Best Local Similarity 47.8%; Pred. No. 5.2e-111;  
 Matches 226; Conservative 73; Mismatches 160; Indels 14; Gaps 10;  
 QY 1 MLGIWIVARLFFGTSRGKVCYERLGCPCDGLPWTSTELVGLPWSPEKINTREFLLYT 60  
 DB 1 MLPFWLGLLLATVAGKEVCYERLGCFSDDSPSGITERPLHLPLWSPKDVNTRFLLYT 59  
 QY 61 IHNPNAYQEISAVNSSTIOASYFGTDKITRINIAGW--KTDGKWORDMNCVLLQLEDINC 118  
 DB 60 NENPNFQEVAA-DSSSISGSNFKTRKTRFIHGFIDKGEENMLANVCNLFKVESVNC 118  
 QY 119 INLDWINGSRE-YIHAVNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGSLGAHLAGEA 177  
 DB 119 ICVDWHRGSRITGTCASQNIIRIVGAEVAFVEFLQSAFYSPSNVHVHIGSLGAHLAGEA 178  
 QY 178 GSRIPG-LGRITGLDPAGFPFHNTPREVRLDPSDANFVDVIHTNAARILFELGVGTIDAC 236  
 DB 179 GRTNGTIGRITGLDPAPFCQGTPELVRLDPSDAKEFVDVIHTDGAIVPNLGFMSQV 238  
 QY 237 GHLDFFPNGKHEMPCGEDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESILNPDAF 296  
 DB 239 GHLDFFPNGGVEMPCCKNVLISOI-VIIDGIWEGTRDPAACNHLRSKYKYTDSIVNPDGF 297  
 QY 297 IAYPCRSYTSFKAGNCFKCEGCPMTGHFADRFHFKMKTN--GSHYFLNTGSLSPFAR 354  
 DB 298 AGFPCCASVNVFTANKPCPCSGCGCPQMGHYADRY---PGKTNDVGQKCYLCTGDASNFA 354  
 QY 355 WHKLSVKLSGSEVTOGTVFLRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVNGNIT 414  
 DB 355 WRYKVSVTLSGKKVT-GHILVSLFNGKNSKQYBIFKGLTKPOSTHNEFDSDVDVGDQLQ 413  
 QY 415 SVQFTWKXHLFPEDSQNKLAGEMVINTSGKYKSTFCSDQIMGNILQNLKPC 467  
 DB 414 MVKFIWNNVINPTLPRVGASKII-VETNKGQNFQCSPEVREEVLLTLTPC 465  
 RESULT 9  
 US-09-411-132A-6  
 ; Sequence 6, Application US/09411132A  
 ; Patent No. 6558936  
 ; GENERAL INFORMATION:



PILICANT: Khodadoust, Mehran  
PILICANT: Kapeller-Liebermann, Rosana  
FILE OF INVENTION: No. 65893661 Human Lipase Proteins, Nucleic Acids Encoding  
FILE OF INVENTION: Them, and Uses of Both of These  
LE REFERENCES: 10147-14  
RENT APPLICATION NUMBER: US/09/411,132A  
RENT FILING DATE: 2000-09-12  
MBER OF SEQ ID NOS: 10  
FWARE: Patent in Ver. 2.1  
ID NO 6  
ENGTH: 465  
YPE: PRT  
GANISM: Homo sapiens  
-411-132A-6

ry Match 44.1%; Score 1115; DB 4; Length 465;  
- Local Similarity 47.8%; Pred. No. 5.2e-111;  
-hes 226; Conservative 73; Mismatches 160; Indels 14; Caps 10;

1 MLGIWIVAVLFEGTSGKEVCYVERLGCDFKDGLPWTRTFSTELVCLPWSPEKINTRLFLYT 60  
1 MLPLWTL5-LLLGAVAGKEVCYVERLGCDFSDSPSGGTERPLPHLPSPKDVNTRLFLYT 59  
61 IHPNAYQBSISAVNSTIQASVFGTDKTRINIAGW--KTDGKWORDCMNVLQLQLEDINC 118  
60 NENPNNFQEVAA-DSSISG5NFKNRKTFRILHGFIDKGEENWLANVCNLPKVESVNC 118  
119 INLDWINGSR-EYIHAVNLRVVGAEVAYFIDVLMKFEYSKPKHLIGHSLCAHLAGEA 177  
119 ICVDWGGSGRTGTQASQIRIVGAEVAYFEVFCQSAFGYSPSNVHVIHSLGAHAAGEA 178  
178 GSRIPG-LGRITGLDPA9PFFHNTPEKVELRDP5DANFVDVIHNTAARILFELGVGTIDAC 236  
179 GRTNGTIGRITGLDPA9PCFQGTTELVRLDPSDAKEVDVHITDGAIPVNLGFGNSQTV 238  
237 GHLDFTPNGKMPGCCEDLITPLKFNPNAYKKEMASFFDCNARSYQVFA5SILNPDAF 296  
239 GHLDFTPNGGVMPCGCKNLSQI-VDIDGIEWEGRDFAACNHLRSYKYVTD5IVNPDGF 297  
297 IAYPCRSYTSFKAGNCFKSGKEGCPQMCHGFADRFHFKNMKTIN--GSHYFLNTGSLSPRAR 354  
298 AGFFCASYNVFTANKCFPCSGCGCPQMCHYADRY---PGKTDVGGQKFLYLDTDGASNFAR 354  
355 WRHKL5VKLGGSEVTQGTVFLRVGGAIGKTGEFAIV5GKLEPGMTYTKLIDADVNVGNIT 414  
355 WRYKVSVTLSGKKVT-GHIL5LFGNKENSQXEIPIKGTLPKDPSTHSNEFSDVDVGDLDQ 413  
415 SVQFIWKHKLFPDSQNKLAGENVINTSKYGYKSTFCSDQIMGFNLIQNLKPC 467  
414 MKRFYINNVNPTLRVGASKII-VETNWKQPNFCSPETVREEVLLTLTPC 465

7 10  
-985-492-14  
ence 14, Application US/08985492  
ent No. 639530  
ERAL INFORMATION:  
APPLICANT: Jaye, Michael C.  
APPLICANT: Doan, Kim-Anh T.  
APPLICANT: Krawiec, John A.  
APPLICANT: Lynch, Kevin J.  
APPLICANT: Amin, Dilip V.  
APPLICANT: South, Victoria J.  
FILE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
FILE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
FILE OF INVENTION: IN ENZYMATIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd. 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA

```

; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,492
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehner Ph.D., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: A2582-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-985-492-14

Query Match 21.1%; Score 534; DB 4; Length 499;
Best Local Similarity 33.3%; Pred. No. 2e-48;
Matches 145; Conservative 64; Mismatches 183; Indels 44; Gaps 14;

QY 51 KINTRFLLYTHNPNAYQISAVNSSTIQASVFGTDKITRINIAGWKTDGK-----WORD 105
DB 47 EMKTRFLLEGTNQGC--QIRINHPTDLOECGFNSSLPLVMIHGWSDGVLENMTWQMV 104
QY 106 MCNVLLQLEDINCINLDWINGSRE-YIHAVNLRVVGAEVAFIDVLAKKFEYSPSKVHL 164
DB 105 AALKSQPAPVNVGLVDWITLAHDHVTIAVRNTRLVGKEVAALLRWLESSVQLSRSHVHL 164
QY 165 IGHSGLCAHLAGEAGSRIPG---LGRITGLDPAQPPFHNTPFKEVRLDPSDANFVDVHTNA 221
DB 165 IGVSLGAHVSGFAGSGIGGTHKIGRTGLDAAGPLFEGSAPSNRLSPDDANFVDAIHT-F 223
QY 222 ARLLFLGLVGTDDACHLDFYNGXHMFGCB--DLITELLKFNFNAYKKEVASFFDCNH 279
DB 224 TREHMLGVGIKQPIGHYDFYPNGGSGFQPGCHFLRYHRIAQGFNA----ITQTIKCSH 279
QY 280 ARSYQFYASIIINPDA-FIAYPCRSYTSFKAGNCFSCKEGQPTMGHFADRFHK-NMKT 337
DB 280 ERSVHLFIDSLHAGTQSMAYFCGDWNSFSQGLCLSCKGRNTLG-----YAVRQEPS 334
QY 338 NGSHYFLNTGSLSPFARWRHKL SVLKS GSEVT--QQTVELRVGGAGIKGTGEFAIVSGK-L 394
DB 335 KSKRFLVTRAOSPPRVVHYQLKIOPINOTETPIQTFTTMSLLGTKEKMQKIPITLGKGI 394
QY 395 EPGMTYTKLIDAVNVGNITSVQFTWK-----KHLFEOSQNLGAEMWINT-- 440
DB 395 ASNKTYFSFLITDLDIGELIMIKFKWENSAMVANWVDVTQTIIPWSTGPRHSLGLVLTIR 454
QY 441 --SGKYGYKSTFCSD 454
DB 455 VRAGETQQRMTFCSEN 470

RESULT 11
US-08-985-492-8
; Sequence 8, Application US/08985492
; Patent No. 6395530
; GENERAL INFORMATION:
; APPLICANT: Jaye, Michael C.
; APPLICANT: Doan, Kim-Anh T.
; APPLICANT: Krawiec, John A.
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Amin, Dilip V.

```

APPLICANT: South, Victoria J.  
TITLE OF INVENTION: LIG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
TITLE OF INVENTION: IN ENZYMATIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd. 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,492  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehlner Ph.D., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: A2582-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610)454-3839  
TELEFAX: (610)454-3808  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
J-985-492-8

ary Match 20.4%; Score 515.5; DB 4; Length 500;  
at Local Similarity 31.2%; Pred. No. 1.9e-46;  
:ches 152; Conservative 72; Mismatches 178; Indels 85; Gaps 22;  
20 VCYERLCGKDFGKPLWTRFTSTELVGLPWSPE-----KINTRELLYTIH 62  
13 LCY-----CFAAGSP-----VFPGEGRLEDKHKPKATQTEVKPSVRENLRATSK 57  
63 NP---NAYQEIISAVNSTIQASYFGTDKITRINAGWKTDG---KWQDMCNVLLQLE-D 115  
58 DPEHEGCV--LSVGHSGQLEDCSFNWTAKTFFIIHGTWMSGIFENWHLKLSALHTREKD 115  
116 INCINLDWINGSRE-YIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLA 174  
116 ANVVVDWDLPLAHLQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVA 175  
175 GEAGSRIPG-LGRITGLDPAGPFPHNTPEKVRLDPSDANFVDVIHTNAARILFELGVGTI 233  
176 GYAGNFVKGTGVRITGLDPAGPFEGADIHKRLSPDDADFDVLHTYTRS--FGLSIGIQ 233  
234 DACGHLDFYPNGKHPGCG--EDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESIL 291  
234 MPVGHIDIYPNGDFQPGGLNDVLGSI-----AY-GTITEVVKCEHERAVHLFVDSL 286  
292 NPD-AFTAYPCRYTSFKAGNCFSCKEGCPVGHFADPHFKNMKTNGSHVFLNTGSL 350  
287 NQDKPSFAFOCTDSNRFKGCICLSCKRNCNSIGYNAKQVRNK---RNSKMYLXTRAGM 342  
351 PFAAWR-----HKLSVKLSGSEVTQGVFLRVGG--AIGKTGEFAVSGKLPFGMTYTKL 403  
343 PFRVYHYQMKIHVFSYKNWGE--IETFFVYLTGTNADSCQTLPLEIVE-RIQONATN 399  
404 IDADVNGNITSVQFIWK-----KHLFEDSQNKL-----GAEMVIN-----TSKYGYK 447  
400 VYTEEDLGDLKILQLTWEGASQSWYNLWKEFRSYLSQPRNPGKELNIRIRVKSGETQK 459  
448 STFCSD 454

Db 460 LIFTED 466  
RESULT 12  
US-08-985-492-10  
Sequence 10, Application US/08985492  
Patent No. 6395530  
GENERAL INFORMATION:  
APPLICANT: Jaye, Michael C.  
APPLICANT: Doan, Kim-Anh T.  
APPLICANT: Krawiec, John A.  
APPLICANT: Lynch, Kevin J.  
APPLICANT: Amin, Dilip V.  
APPLICANT: South, Victoria J.  
TITLE OF INVENTION: LIG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
TITLE OF INVENTION: IN ENZYMATIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd. 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,492  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehlner Ph.D., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: A2582-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610)454-3839  
TELEFAX: (610)454-3808  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-985-492-10  
Query Match 18.3%; Score 462.5; DB 4; Length 345;  
Best Local Similarity 34.0%; Pred. No. 5.2e-41;  
Matches 123; Conservative 46; Mismatches 134; Indels 59; Gaps 15;  
Qy 20 VCYERLCGKDFGKPLWTRFTSTELVGLPWSPE-----KINTRELLYTIH 62  
Db 13 LCY-----CFAAGSP-----VFPGEGRLEDKHKPKATQTEVKPSVRENLRATSK 57  
Qy 63 NP---NAYQEIISAVNSTIQASYFGTDKITRINAGWKTDG---KWQDMCNVLLQLE-D 115  
Db 58 DPEHEGCV--LSVGHSGQLEDCSFNWTAKTFFIIHGTWMSGIFENWHLKLSALHTREKD 115  
Qy 116 INCINLDWINGSRE-YIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLA 174  
Db 116 ANVVVDWDLPLAHLQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVA 175  
Qy 175 GEAGSRIPG-LGRITGLDPAGPFPHNTPEKVRLDPSDANFVDVIHTNAARILFELGVGTI 233  
Db 176 GYAGNFVKGTGVRITGLDPAGPFEGADIHKRLSPDDADFDVLHTYTRS--FGLSIGIQ 233  
Qy 234 DACGHLDFYPNGKHPGCG--EDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESIL 291  
Db 234 MPVGHIDIYPNGDFQPGGLNDVLGSI-----AY-GTITEVVKCEHERAVHLFVDSL 286

292 NPD-AFIAYPCRSYTSFKAGNCFKSCKEGCTMGHFAFRPHFKMKTNGSHYFLNTGSL 350  
 287 NODKPSFAFQCTDSNRFFKKGICLSCKRNCNSIGYNAKVRNK-----RNSKMYLKTRAGM 342  
 351 PF 352  
 343 PF 344

r 13

-985-492-4  
 jence 4, Application US/08985492  
 sent No. 6395530  
 VERAL INFORMATION:  
 APPLICANT: Jaye, Michael C.  
 APPLICANT: Doan, Kim-Anh T.  
 APPLICANT: Krawiec, John A.  
 APPLICANT: Lynch, Kevin J.  
 APPLICANT: Amin, Dilip V.  
 APPLICANT: South, Victoria J.  
 TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
 TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
 TITLE OF INVENTION: IN ENZYMIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 STREET: 500 Arcola Rd. 3C43  
 CITY: Collegeville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,492  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fehner Ph.D., Paul F.  
 REGISTRATION NUMBER: 35,135  
 REFERENCE/DOCKET NUMBER: A2582-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610)454-3839  
 TELEFAX: (610)454-3808  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 353 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -985-492-4

Query Match 18.3%; Score 462.5; DB 4; Length 353;  
 Best Local Similarity 34.0%; Pred. No. 5.4e-41;  
 Matches 123; Conservative 46; Mismatches 134; Indels 59; Gaps 15;  
 20 VCVERLGCDFKGLPWTRTFSTELVGLPWSPE-----KINTRFLLYTH 62  
 13 LCY-----CFAAGSP-----VPFGEGLEDKHLKPKATQTEVPSVRFNLRISK 57  
 63 NP---NAYQEISAVNSSTIOASYFGTDKTRINIAWKTDG---KQWRDMCNVLLQLE-D 115  
 58 DPEHEGCV--LSVGHSPLEDCPSFNMTAKTFIIGHWTMSGIFENWLKLVSAHTRKD 115  
 116 INCINLDWINGSRE-YHAVNNLVGAEVAYTIDVLKMFYSPKSVHLIGSLGAHLA 174  
 116 ANVVVDVWLPALHQLYTDVANNTRVWGHGSIARMLDWLQEKDPSLGNVHLIGSLGAHVA 175  
 175 GEAGSRIPG-LGRITGLDPAGFPFHTPKVRLDPSDANVDVHTNAAILFELGVGTI 233

Db 176 VGAGNFVKGTVGRITGLDPAGPMEGADIHKRLSPDDADFDVVLHTVTRS--FCLSLGIQ 233  
 QY 234 DACGHLDYPPNGGKHMGC--EDLITPLKFNAYKEMASPFDCNHARSYQFYAESIL 291  
 Db 234 MEVGHIDIYPNGGDFQPGCGLNDVLGSI-----AY-GTITEVVKCEHERAVHLFVDSL 286  
 QY 292 NPD-AFIAYPCRSYTSFKAGNCFKSCKEGCTMGHFAFRPHFKMKTNGSHYFLNTGSL 350  
 Db 287 NODKPSFAFQCTDSNRFFKKGICLSCKRNCNSIGYNAKVRNK-----RNSKMYLKTRAGM 342  
 QY 351 PF 352  
 Db 343 PF 344

RESULT 14

US-08-985-492-6  
 Sequence 6, Application US/08985492  
 Patent No. 6395530  
 GENERAL INFORMATION:  
 APPLICANT: Jaye, Michael C.  
 APPLICANT: Doan, Kim-Anh T.  
 APPLICANT: Krawiec, John A.  
 APPLICANT: Lynch, Kevin J.  
 APPLICANT: Amin, Dilip V.  
 APPLICANT: South, Victoria J.  
 TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
 TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
 TITLE OF INVENTION: IN ENZYMIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 STREET: 500 Arcola Rd. 3C43  
 CITY: Collegeville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,492  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fehner Ph.D., Paul F.  
 REGISTRATION NUMBER: 35,135  
 REFERENCE/DOCKET NUMBER: A2582-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610)454-3839  
 TELEFAX: (610)454-3808  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 354 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-985-492-6

Query Match 18.3%; Score 462.5; DB 4; Length 354;  
 Best Local Similarity 34.0%; Pred. No. 5.4e-41;  
 Matches 123; Conservative 46; Mismatches 134; Indels 59; Gaps 15;  
 20 VCVERLGCDFKGLPWTRTFSTELVGLPWSPE-----KINTRFLLYTH 62  
 13 LCY-----CFAAGSP-----VPFGEGLEDKHLKPKATQTEVPSVRFNLRISK 57  
 63 NP---NAYQEISAVNSSTIOASYFGTDKTRINIAWKTDG---KQWRDMCNVLLQLE-D 115  
 58 DPEHEGCV--LSVGHSPLEDCPSFNMTAKTFIIGHWTMSGIFENWLKLVSAHTRKD 115

116 INCINLDWINGSRE-YIHAVNNLRVGAEVAFIDVLMKKFSPSKVHLIGHSLGAHLA 174  
 116 ANVVVDWLPLAHQLYTDVANNTRVVGHSIARMLDWLQEKDFDSLGNVHLIGYSLGAHVA 175  
 175 GEASRIPLG-LGRITGLDPAGPFPHHTPKVRLDPDANFVDVHTNNAARILFELGVGTI 233  
 176 GYAGNFYKGTGVRITGLDPAGPMFEGADIHKRLSPDDADFDVLTHTYTRS--FGLSIGIQ 233  
 234 DACGHLDFYNGGKHMFGC--EDLIITPLKFNENAYKEMASFFDCNHNARSYQFVAESIL 291  
 234 MPVGHIDIYNGGDFQFGGLNDVLSI-----AY-GTITEVKCEHERAVHLFVDSIV 286  
 292 NPD-AFTAYPCRSYTSKAGNCFCSKEGCPWGHFADRFHFNKMKNGSHYFLNTGSL 350  
 287 NQDKPSFAFOCTDSNRFKKGICILSCRKNCISGYNAKVRNK----RNSKMYLXTRAGM 342  
 351 PF 352  
 343 PF 344

JT 15  
 8-985-492-13  
 pence 13, Application US/08985492  
 ent No. 6395530  
 INERAL INFORMATION:  
 APPLICANT: Jaye, Michael C.  
 APPLICANT: Doan, Kim-Anh T.  
 APPLICANT: Krawiec, John A.  
 APPLICANT: Lynch, Kevin J.  
 APPLICANT: Amin, Dilip V.  
 APPLICANT: South, Victoria J.  
 TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
 TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
 TITLE OF INVENTION: IN ENZYMIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 STREET: 500 Arcola Rd. 3043  
 CITY: Collegeville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,492  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fehner Ph.D., Paul F.  
 REGISTRATION NUMBER: 35,135  
 REFERENCE/DOCKET NUMBER: A2582-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610)454-3839  
 TELEFAX: (610)454-3808  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 472 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 985-492-13

ry Match 17.4%; Score 440.5; DB 4; Length 472;  
 t Local Similarity 28.1%; Pred. No. 2.1e-38;  
 ches 127; Conservative 79; Mismatches 195; Indels 51; Gaps 16;

QY 34 WRTFTELVGLPWPSEK-----INTRFLLYTHNPAYQE-----ISAVNSSTIQASYF 83  
 Db 14 WQSLTASRGVAAADQDRDFIDIESKALRT---PETAEDTCHLIPGV-AESVATCHF 69  
 QY 84 GTDKITRINIAGWKTDG---KWQDMCNVLQLE-DINCINLDWINGSREYIHAVNNLRV 139  
 Db 70 NHSSKTFMWIHGWTVTGMYESWVVKLVAALKYKRPDSNVIVDWLSRAQEHYVPVSAGYTK 129  
 QY 140 VQAEVAYFDVLMKKFSPSKVHLIGHSLGAHLAGEAGSRI-PGLGRITGLDPAGPF 198  
 Db 130 VGODVARFINWMEEFNPLDNVHLGYSLGAHAGIAGSLTNKKVNRITGLDPAGNFE 189  
 QY 199 NTPKEVRLDPDANFVDVHTNNAARILFELG-----VGTIDACGHLDFYPNGGKHMFGCE 253  
 Db 190 YA-EAPRLSPDDADFDVLTHT-----FTRGSPGRSIGIQKPVGHVDIYPNGGTFQPGCN 242  
 QY 254 --DLITPLKFNENAYKEMASFFDCNHNARSYQFVAESILNPD-AFTAYPCRSYTSFKAG 310  
 Db 243 IGEAIRVIAERGLGDVQ-----LCSHERSIHLFIDSLNEENPSPKAYRCSKEAFKG 297  
 QY 311 NCFPCSKGECPTMGHFADRFHFNKMKNGSHYFLNTGSLSPFARWRHKLKSLGSEV-- 368  
 Db 298 LCLSCRKNRCNNLGYEINKVRK-----RSSKMYLXTRSQMPYKVFHYQVKIHFSGTSET 353  
 QY 369 -TQGTVFLEVGAIGKTGEPAIVSGKLEPGMTYTKLIDADVNVGNITSVQFIWKHLFED 427  
 Db 354 HTNQAFETSLYGTVAESENIPFTLPEVSTNKTYSFLIYTEVDIGELLMLKLKWKSDSYFS 413  
 QY 428 -----SQNLGAEMVINTSGKYGYKSTFCSDQ 454  
 Db 414 WSDMWSPPGFAIQKIRVKAGETQKKVIFCSRE 445

Search completed: January 6, 2004, 11:24:08  
 Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

rotein - protein search, using sw model

n: January 6, 2004, 08:50:18 ; Search time 51 Seconds  
(without alignments)  
1453.437 Million cell updates/sec

US-10-038-517-2

ct score: 2527

nce: 1 MLGIWIVAFLEFGTSGKEV.....STFCSQDMGNILQNLKPC 467

ng table: BLOSUM62

Gapop 10.0 , Gapext 0.5

hed: 1107863 seqs, 158726573 residues

number of hits satisfying chosen parameters: 1107863

um DB seq length: 0

um DB seq length: 2000000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

ase : A Geneseq 19Jun03:\*

1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
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8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.\*  
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22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score	Query Match	Length	ID	Description
2527	100.0	467	23	ABB77987
2527	100.0	467	23	ABB79039
2523	99.8	467	22	AAE00508
2276	90.1	461	23	AAE17302
1937	76.7	368	23	ABB08004
1878.5	74.3	462	23	ABB53289
1456	57.6	276	23	ABB97589
1191	47.1	469	23	ABB79040
1180	46.7	467	23	ABB79041

10	1172	46.4	467	23	ABB79042	Rat pancreatic lip
11	1162	46.0	467	23	ABB06317	Plrpl amino acid s
12	1159	45.9	470	14	AAE03741	GPI(+/-) mutant with
13	1156	45.7	452	14	AAE03737	Guinea pig pancrea
14	1152	45.6	469	22	ABG16896	Novel human diagno
15	1152	45.6	469	23	ABB06318	Plrpl2 amino acid s
16	1152	45.6	477	21	AAE54287	Human pancreatic c
17	1143.5	45.3	474	22	ABG16895	Novel human diagno
18	1115	44.1	465	23	ABB06321	Human lipase amino
19	1115	44.1	465	23	AAU87690	Human pancreatic t
20	1115	44.1	473	21	AAE54115	Human pancreatic c
21	1091.5	43.2	450	14	AAE03738	Human pancreatic l
22	1088.5	43.1	432	14	AAE34294	HPL(-/-) mutant with
23	980	38.8	392	21	AAE00075	Human secreted pro
24	899.5	35.6	336	14	AAE030740	C-terminally truca
25	886.5	35.1	470	22	ABG16892	Novel human diagno
26	886	35.1	319	14	AAE030739	C-terminally trunc
27	879.5	34.8	336	14	AAE34293	C-terminally trunc
28	866	34.3	319	14	AAE34292	C-terminally trunc
29	555.5	22.0	952	22	ABB62733	Drosophila melanog
30	534	21.1	498	23	ABB06319	Lipase amino acid
31	534	21.1	499	23	AAO15887	Human hepatic lipa
32	525	20.8	500	20	AAE23760	Mouse endothelial
33	515.5	20.4	452	23	AAE17316	Human lipase prote
34	515.5	20.4	500	19	AAE59792	Amino acid sequenc
35	515.5	20.4	500	20	AAE23759	Human endothelial
36	515.5	20.4	500	21	AAE19178	Human LIPG, a tria
37	515.5	20.4	500	23	AAO14635	Human lipase endot
38	515.5	20.4	500	24	ABU03569	Angiogenesis-assoc
39	513	20.3	451	22	AAE10996	Human lipid metabo
40	513	20.3	451	22	AAE73560	Human lipase 18892
41	513	20.3	451	23	ABB06316	Human phospholipas
42	513	20.3	451	24	ABU08952	Human novel lipase
43	500	19.8	540	22	ABB61963	Drosophila melanog
44	462.5	18.3	345	19	AAE59793	Amino acid sequenc
45	462.5	18.3	345	21	AAE19179	The catalytic doma

#### ALIGNMENTS

##### RESULT 1

ABB77987

ID ABB77987 standard; Protein, 467 AA.

XX ABB77987;

XX

DT 22-OCT-2002 (first entry)

DE Amino acid sequence of a human lipase.

XX Human; lipase; enzyme; mental disorder; disease; gene.

XX Homo sapiens.

XX WO200253753-A2.

XX 11-JUL-2002.

XX 03-JAN-2002; 2002WO-US00223.

XX 05-JAN-2001; 2001US-259830P.

XX (LEXI-) LEXICON GENETICS INC.

XX Yu X, Turner CA;

XX WPI; 2002-583623/62.

XX N-PSDB; ABL59436.

XX Nucleic acid molecule encoding a human lipase, useful in therapeutic, diagnostic and pharmacogenomic applications, as DNA markers for restriction fragment length polymorphism analysis and in forensic

biology -

Claim 4; Page 35-36; 36pp; English.

The present sequence represents a human lipase polypeptide. The lipase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenomic applications, and for identifying compounds that modulate, i.e., act as agonists or antagonists of the gene expression or gene product activity. They are also useful in the human lipase protein gene regulation and/or as antisense primers in amplification reactions of the nucleic acid sequences, for detecting mutant human proteins or inappropriately expressed proteins for the diagnosis of disease, for screening for drugs effective in treating the symptomatic or phenotypic manifestations of perturbing the normal function of the protein in the body, for generating transgenic animals and antibodies, for identifying other cellular gene products related to the protein, and as reagents in assays for screening for compounds that can be used as pharmaceutical agents in the therapeutic treatment of mental, biological or medical disorders and diseases.

Sequence 467 AA;

Query Match 100.0%; Score 2527; DB 23; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-244;  
 Mismatches 0; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MLGIWIVAFPGTSRGKVCYERLGCDFDGLPWTFTSTELVGLPWSPEKINTRFLLYT 60  
 1 MLGIWIVAFPGTSRGKVCYERLGCDFDGLPWTFTSTELVGLPWSPEKINTRFLLYT 60  
 61 IHNPNAYQEISAVNSSTIQASYFGTDKITRINAGWKTDGKQWDMCNVLLQLEDINCIN 120  
 61 IHNPNAYQEISAVNSSTIQASYFGTDKITRINAGWKTDGKQWDMCNVLLQLEDINCIN 120  
 121 LDWINGSREYIHAVNNLRVVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180  
 121 LDWINGSREYIHAVNNLRVVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180  
 181 IPGLGRITGLDPAGPFFHNTPEKVRLPDSDANFVDVHTNAARILFELGVGTIDACGHL 240  
 181 IPGLGRITGLDPAGPFFHNTPEKVRLPDSDANFVDVHTNAARILFELGVGTIDACGHL 240  
 241 FYPNGGKHPGCCDLITPLLKFNFNAYKEMASFFDCNARSYQFYAESILNPDFAIAYP 300  
 241 FYPNGGKHPGCCDLITPLLKFNFNAYKEMASFFDCNARSYQFYAESILNPDFAIAYP 300  
 301 CRSYTSFKAGNCFPCSKGECPTMGHFDAPRHFKNMKTNGSHYFLNTGSLSPFARWRHKL 360  
 301 CRSYTSFKAGNCFPCSKGECPTMGHFDAPRHFKNMKTNGSHYFLNTGSLSPFARWRHKL 360  
 361 VKLSGSEVTQGTVFLRVGGAIGKTGEFAIVSGKLBPGMTYTKLIDADVNVGNITSVQFIW 420  
 361 VKLSGSEVTQGTVFLRVGGAIGKTGEFAIVSGKLBPGMTYTKLIDADVNVGNITSVQFIW 420  
 421 KXHLFEDSQNKLGAEMVINTSGKYGYKSTFCSDQIMGNILQNLKPC 467  
 421 KXHLFEDSQNKLGAEMVINTSGKYGYKSTFCSDQIMGNILQNLKPC 467

T 2  
 039

ABB79039 standard; Protein; 467 AA.

01-AUG-2002 (first entry)

Human lipase protein sequence SEQ ID NO:2.

Human; lipase; enzyme; therapeutic.

Homo sapiens.

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US2002052034-A1.

02-MAY-2002.

14-DEC-2000; 2000US-0735933.

28-SEP-2000; 2000US-235925P.

(GUEG/) GUEGLER K.

(WEBB/) WEBSTER M.

(KETCH/) KETCHUM K A.

(DFRA/) DI FRANCESCO V.

(BEAS/) BEASLEY E M.

Guegler K, Webster M, Ketchum KA, Di Francesco V, Beasley EM;

WPI; 2002-443697/47.

N-PSDB; ABN97363, ABN97364.

A lipase protein identified from the human genome is related to the

pancreatic lipase subfamily, and is useful to provide new drug targets

in the discovery of therapeutics for lipase-mediated disease

Claim 1; Fig 2; 85pp; English.

The present sequence represents a human lipase protein. Molecules from

the present invention can be used as models for the development of human

therapeutic targets, aid in the identification of therapeutic proteins

and serve as targets for the development of human therapeutic agents

that modulate lipase activity in cells and tissues that express lipase.

Sequence 467 AA;

Query Match 100.0%; Score 2527; DB 23; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.8e-244;

Mismatches 0; Indels 0; Gaps 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLGIWIVAFPGTSRGKVCYERLGCDFDGLPWTFTSTELVGLPWSPEKINTRFLLYT 60

1 MLGIWIVAFPGTSRGKVCYERLGCDFDGLPWTFTSTELVGLPWSPEKINTRFLLYT 60

61 IHNPNAYQEISAVNSSTIQASYFGTDKITRINAGWKTDGKQWDMCNVLLQLEDINCIN 120

61 IHNPNAYQEISAVNSSTIQASYFGTDKITRINAGWKTDGKQWDMCNVLLQLEDINCIN 120

121 LDWINGSREYIHAVNNLRVVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180

121 LDWINGSREYIHAVNNLRVVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180

181 IPGLGRITGLDPAGPFFHNTPEKVRLPDSDANFVDVHTNAARILFELGVGTIDACGHL 240

181 IPGLGRITGLDPAGPFFHNTPEKVRLPDSDANFVDVHTNAARILFELGVGTIDACGHL 240

241 FYPNGGKHPGCCDLITPLLKFNFNAYKEMASFFDCNARSYQFYAESILNPDFAIAYP 300

241 FYPNGGKHPGCCDLITPLLKFNFNAYKEMASFFDCNARSYQFYAESILNPDFAIAYP 300

301 CRSYTSFKAGNCFPCSKGECPTMGHFDAPRHFKNMKTNGSHYFLNTGSLSPFARWRHKL 360

301 CRSYTSFKAGNCFPCSKGECPTMGHFDAPRHFKNMKTNGSHYFLNTGSLSPFARWRHKL 360

361 VKLSGSEVTQGTVFLRVGGAIGKTGEFAIVSGKLBPGMTYTKLIDADVNVGNITSVQFIW 420

361 VKLSGSEVTQGTVFLRVGGAIGKTGEFAIVSGKLBPGMTYTKLIDADVNVGNITSVQFIW 420

421 KXHLFEDSQNKLGAEMVINTSGKYGYKSTFCSDQIMGNILQNLKPC 467

RESULT 3  
 AAB00508  
 ID AAB00508 standard; Protein; 467 AA.

AAE00508;

13-JUN-2001 (first entry)

Human lipase protein, MLip-1.

Human, lipase; MLip-1; antiinflammatory; antilipemic; cardiant; therapy; anorectic; cholesterol biosynthesis; lipid metabolism; diabetes; obesity; pancreatic disorder; nutritional disorder; malabsorption; malnutrition; metabolic disorder; hyperlipidemia; hypolipidemia; abdominal lesion; lipidoses; pancreatic duct obstruction; Gaucher's disease; peritonitis; atherosclerosis; Niemann-Pick disease; arteriosclerosis; pancreatitis; coronary artery disease; perforated peptic ulcer; intestinal obstruction; linoleic acid deficiency.

Homo sapiens.

Key Location/Qualifiers

1..17

/label= Signal\_peptide

13..18

/note= "N-myristoylation site"

Protein

18..467

/label= Human\_mature\_MLip-1\_lipase\_protein

Modified-site

31..36

/note= "N-myristoylation site"

Domain

42..343

/label= Lipase domain

/note= "Involved in the formation and hydrolysis of one or more ester bonds of mono-, di- and tri-glycerides"

Modified-site

74..77

/label= Asn is N-glycosylated

Modified-site

125..128

/label= Asn is N-glycosylated

Modified-site

141..146

/note= "N-myristoylation site"

Active-site

162..171

/label= Lipase\_serine\_active\_site

Modified-site

170..175

/note= "N-myristoylation site"

Modified-site

189..194

/note= "N-myristoylation site"

Modified-site

231..236

/note= "N-myristoylation site"

Modified-site

338..341

/label= Asn is N-glycosylated

Domain

355..467

/label= PLAT/LH2\_domain

/note= "Mediate association of protein with membranes and lipid vesicles"

Modified-site

365..370

/note= "N-myristoylation site"

Modified-site

378..383

/note= "N-myristoylation site"

Modified-site

397..402

/note= "N-myristoylation site"

Modified-site

411..416

/note= "N-myristoylation site"

Modified-site

412..415

/label= Asn is N-glycosylated

Modified-site

439..442

/label= Asn is N-glycosylated

PA (MILL-) MILLENIUM PHARM INC.

XX

XX Khodadoust M, Kapeller-libermann R;

XX

DR WPI: 2001-266302/27.

DR

XX N-PSDB; AAD03848.

XX

Novel isolated lipase, MLip-1, useful for identifying compounds which modulate MLip-1 activity, for treating conditions or disorders associated with aberrant activity of MLip-1 such as hypolipidemia, obesity

XX

PS Claim 9; Fig 1; 112pp; English.

XX

The present sequence is human lipase protein, MLip-1. MLip-1 catalyse the formation and cleavage of ester bonds between fatty acyl moieties and glyceride moieties. It is involved in dietary fat degradation and absorption, cholesterol biosynthesis and maintenance of plasma lipid and lipoprotein levels. MLip-1 is also useful for identifying compounds which modulates its activity and expression. These compounds are useful for preventing, diagnosing or treating disorders relating to inappropriate lipid metabolism and aberrant pancreatic function such as diabetes, obesity, nutritional disorders (e.g. lipid malabsorption and malnutrition), metabolic disorders (particularly including lipid metabolism anomalies such as hyperlipidaemia of types I to V and hypolipidaemia), pancreatitis, obstruction of the pancreatic duct, various lipidoses (e.g. Gaucher's disease and Niemann-Pick disease), atherosclerosis, arteriosclerosis, coronary artery disease, perforated peptic ulcer, abdominal lesions, intestinal obstruction, peritonitis and linoleic acid deficiency. MLip-1 and its modulators can be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing and forensic biology assays), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring of clinical trials and pharmacogenomic applications) and methods of treatment (e.g. therapeutic and prophylactic methods).

SQ Sequence 467 AA;

Query Match	99.8%	Score 2523	DB 22	Length 467
Best Local Similarity	99.8%	Pred. No. 9.6e-244		
Matches 466	Conservative 1	Mismatches 0	Indels 0	Gaps 0
QY	1	MLGIWIVAFLEFFGTSRGKVCYERLGC	FDGLPWTFTSTELVGLPWSPEKINTRELLYT	60
Db	1	MLGIWIVAFLEFFGTSRGKVCYERLGC	FDGLPWTFTSTELVGLPWSPEKINTRELLYT	60
QY	61	IHNPNAYOEISAVNSSTIQASYFGTDKI	TRINIAAGWTKDKWQDMCNVLLQLEDINCIN	120
Db	61	IHNPNAYOEISAVNSSTIQASYFGTDKI	TRINIAAGWTKDKWQDMCNVLLQLEDINCIN	120
QY	121	LDWTNGSREYTHAVNNLRVVGAEVAFID	VLMMKFEYSPSKVHLIGHSLCAHLAGEAGSR	180
Db	121	LDWTNGSREYTHAVNNLRVVGAEVAFID	VLMMKFEYSPSKVHLIGHSLCAHLAGEAGSR	180
QY	181	IPGLGRITGLDPAGPPFHTPKVRLDP	SDANFVDVHTNAARILPELGVGTIDACGHLD	240
Db	181	IPGLGRITGLDPAGPPFHTPKVRLDP	SDANFVDVHTNAARILPELGVGTIDACGHLD	240
QY	241	FYPNGGKMPGCCDLITPLKFNFNAYK	KEMASFFDCNHFARSHYQFVAESILNPDAFIAP	300
Db	241	FYPNGGKMPGCCDLITPLKFNFNAYK	KEMASFFDCNHFARSHYQFVAESILNPDAFIAP	300
QY	301	CRSYTSFKAGNCFCSKEGCTMGHFA	DRFHFQNMKNGSHYFLNTGSLSPFARWRHKL	360
Db	301	CRSYTSFKAGNCFCSKEGCTMGHFA	DRFHFQNMKNGSHYFLNTGSLSPFARWRHKL	360
QY	361	VKLSGSEVTQGTFLRVGGAIGTKTG	FAIVSGKLEPGMTYTKLIDADVNVGNITSVQFIW	420
Db	361	VKLSGSEVTQGTFLRVGGAIGTKTG	FAIVSGKLEPGMTYTKLIDADVNVGNITSVQFIW	420
QY	421	KGHLFEDSQNKLGAEMVINTSGKYG	KYKSTFCSDIMGPNILQNLKPC	467
Db	421	KGHLFEDSQNKLGAEMVINTSGKYG	KYKSTFCSDIMGPNILQNLKPC	467

JT 4  
7302

AAE17302 standard; Protein; 461 AA.

AAE17302;

18-APR-2002 (first entry)

Human pancreatic lipase protein, sbg237163LIPASE.

Human; therapy; wound healing disorder; vaccine; cancer; infection; autoimmune disorder; haematopoietic disorder; inflammation; arthritis; Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic; multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma; ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder; depression; cardiovascular disease; myocardial infarction; renal failure; respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder; type II diabetes mellitus; skeletal muscle disorder; immunosuppressive; neoplastic; renal disease; hypoglycaemia; gastrointestinal disease; hypertrophic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory; haemostatic; vulnary; anticoagulant; antirheumatic; neuroprotective; nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective; allergy; pancreatic lipase.

Homo sapiens.

W0200198342-A1.

27-DEC-2001.

22-JUN-2001; 2001WO-US19929.

22-JUN-2000; 2000US-213156P.

22-JUN-2000; 2000US-213161P.

(SMIK) SMITHKLINE BEECHAM CORP.

(SMIK) SMITHKLINE BEECHAM PLC.

(GLAX) GLAXO GROUP LTD.

Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;

Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;

WPI; 2002-139783/18.

N-PSDB; AAD2777.

Novel secreted and membrane-associated polypeptides and polynucleotides useful for preventing, ameliorating or correcting dysfunction or disease including diabetes, cancer, hypertension and growth abnormalities.

Claim 1; Page 99-100; 138pp; English.

The invention relates to secreted and membrane-associated polypeptides and polynucleotides. The sequences of the invention are useful in diagnostic assays for detecting diseases associated with inappropriate activity or levels of these polynucleotides, and in identifying their agonists and antagonists that are potentially useful in therapy. The sequences of the invention are useful as vaccines for inducing immunological response. The sequences of the invention are useful for treating cancers, infections, autoimmune disorders, haematopoietic disorders, wound healing disorders, cholesterol ester storage disease, inflammation, congenital muscular dystrophy, junctional epidermolysis bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis, viral and bacterial infections, Alzheimer's disease, asthma, arthritis, allergies, schizophrenia, sbg424245PROs-associated disorders, septicemia, psoriasis, inflammatory bowel disease, transplant rejection, graft versus host disease, ischaemia, stroke, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis, brain disorders including paraspranuclear palsy, myotonic dystrophy, depression, anxiety disorders and sleep disorders, cardiovascular diseases including congestive heart failure and myocardial infarction,

CC respiratory diseases including chronic obstructive pulmonary disease,  
CC acute bronchitis and adult respiratory distress syndrome, liver disorders  
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral  
CC and non-viral hepatitis, type II diabetes mellitus, renal disease  
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's  
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia  
CC and tendinitis, gastrointestinal diseases including intestinal  
CC obstruction and tropical sprue, spleen disorders including hypersplenism,  
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male  
CC reproductive diseases including low testosterone and male infertility.  
CC The present sequence is human pancreatic lipase.

XX SQ Sequence 461 AA;

Query Match 90.1%; Score 2276; DB 23; Length 461;  
Best Local Similarity 91.5%; Pred. No. 5.5e-219;  
Matches 431; Conservative 8; Mismatches 18; Indels 14; Gaps 3;

QY 1 MGIWIVAFPGTGRGKVCYVERLGCDFGLPWRTPSTELVGLPMSPEKINTRFLLYT 60

Db 1 MGIWIVAFPGTGRGKVCYVERLGCDFGLPWRTPSTELVGLPMSPEKINTRFLLYT 60

QY 61 IHNPNAYQISAVNSSTIQASYFGTDKITRINAGWKTDGKQDMCNVLQLEDINCIN 120

Db 61 IHNPNAYQISAVNSSTIQASYFGTDKITRINAGWKTDGKQDMCNVLQLEDINCIN 120

QY 121 LWINSGREYIHAVNNLRVVGAEVAFIDVLMKKPEYSPKVLHIGSLGAHLAGEAGSR 180

Db 121 LWINSGREYIHAVNNLRVVGAEVAFIDVLMKKPEYSPKVLHIGSLGAHLAGEAGSR 180

QY 181 IPGLGRITGLDPAGPFPHNTPKPEVRLDPSDFVVDVHTNAARILFELGVGTIDACGHL 240

Db 181 IPGLGRITGLDPAGPFPHNTPKPEVRLDPSDFVVDVHTNAARILFELGVGTIDACGHL 240

QY 241 FYPNGGKHPGCCEDLITPLKFNFNAYKKEVAFIDVLMKKPEYSPKVLHIGSLGAHLAGEAGSR 300

Db 241 FYPNGGKHPGCCEDLITPLKFNFNAYKKEVAFIDVLMKKPEYSPKVLHIGSLGAHLAGEAGSR 300

QY 301 CRSYTSFKAGNCFCKSCGCTPMGHFADRFHFKMKTKNGSHVFLNTG----SLSPFARWR 356

Db 301 CRSYTSFKAGTCTV-----GCADLLHRIDK-----IGSTSHVFLTSLPFLVLSLYLGNR 350

QY 357 HKLSVKLSGSEVTQGTFLRVGGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNVGNITSV 416

Db 351 HKLSVKLSGSEVTQGTFLRVGGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNVGNITSV 410

QY 417 QFIWKHLPEDSQNKLGAEMVINTSGKYKSTFCSDIMGNILQNLKPC 467

Db 411 QFIWKHLPEDSQNKLGAEMVINTSGKYKSTFCSDIMGNILQNLKPC 461

RESULT 5

ABB08004

ID ABB08004 standard; Protein; 368 AA.

XX ABB08004;

XX 27-AUG-2002 (first entry)

DE Human lipid metabolism enzyme (LME)-4 (Id: 7482937CD1).

XX Human; lipid metabolism enzyme; LME; cytostatic; neuroprotective;  
XX neurotropic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;  
XX antischlerotic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;  
XX gene therapy; protein therapy; enzyme.

OS Homo sapiens.

XX WO200229036-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US31302.

PF



06-OCT-2000; 2000US-238368P.  
13-OCT-2000; 2000US-240616P.  
02-NOV-2000; 2000US-245719P.  
08-NOV-2000; 2000US-247503P.  
17-NOV-2000; 2000US-249503P.

(INCY-) INCVTE GENOMICS INC.

Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L,  
Wallia NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J,  
Lal PG, Tribouley CM;

WPI: 2002-315862/35.  
N-PSDB; ABL60540.

Lipid Metabolism Enzymes and nucleic acids, useful for preventing,  
diagnosing and treating e.g. cancer, Alzheimer's disease and  
Creutzfeld-Jakob disease -

Claim 1; Page 115-116; 127pp; English.

The invention relates to human lipid metabolism enzymes (LMEs) and  
encoding polynucleotides. The LMEs can be expressed by standard  
recombinant technology. The LME polypeptides, polynucleotides and  
modulators may be used in the prevention, diagnosis and treatment of  
diseases associated with inappropriate LME expression such as cancer  
(e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.  
Parkinson's, Alzheimer's and multiple sclerosis), microbial infections  
(e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome  
(AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina  
pectoris and mitral valve prolapse). The present sequence represents  
the human LME-4 polypeptide.

Sequence 368 AA;

Y Match 76.7%; Score 1937; DB 23; Length 368;

Local Similarity 99.2%; Pred. No. 3.8e-185;  
hes 359; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

106 MCNVLLQLEDINCINLDWINGSREYTHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLI 165

7 LCKVLQLEDINCINLDWINGSRYTHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLI 66

166 GHSGLGAHLAGEAGSRIPGLGRITGLDPAGPFFHNTPKREVLDPDSANFVDVHTNAARIL 225

67 GHSGLGAHLAGEAGSRIPGLGRITGLDPAGPFFHNTPKREVLDPDSANFVDVHTNAARIL 126

226 FELGVGTIDACGHLDPYNGSKHMPGCCEDLITPLLKNFNAYKKEVASPFDCHNARSYQF 285

127 FELGVGTIDACGHLDPYNGSKHMPGCCEDLITPLLKNFNAYKKEVASPFDCHNARSYQF 186

286 YAESILNPDAFIAYPCRSYTSFKAGNCFKSCGCPMGHFADEHFQMKNGSHYFLN 345

187 YAESILNPDAFIAYPCRSYTSFKAGNCFKSCGCPMGHFADEHFQMKNGSHYFLN 246

346 TGSLSPPFARWHRKLSVKLSGSEVTQGTVFLRVGAIGKTBGEFAIVSGKLEPGMTYTKLID 405

247 TGSLSPPFARWHRKLSVKLSGSEVTQGTVFLRVGAIGKTBGEFAIVSGKLEPGMTYTKLID 306

406 ADVNVGNITSYQFIWKKHLFEDSONKLGAEWVINTSGYKSTFCSDQIMGNILONLK 465

307 ADVNVGNITSYQFIWKKHLFEDSONKLGAEWVINTSGYKSTFCSDQIMGNILONLK 366

466 FC 467

367 FC 368

. 6  
89

AB53289 standard; Protein: 462 AA.

AC ABB53289;

XX 12-FEB-2002 (first entry)

DE Human polypeptide #29.

XX Human; nootropic; neuroprotective; anticonvulsant; antidepressant;  
KW neuroleptic; tranquiliser; antiarrhythmic; cardiac; antiasthmatic;  
KW antiinflammatory; antilipemic; hepatotropic; virucide; antidiabetic;  
KW nephrotropic; anorectic; cytostatic; vaccine; neurologic disease;  
KW cardiovascular disease; respiratory disease; liver disease;  
KW renal disease; skeletal muscle disease; gastrointestinal disease;  
KW placental disease; testicular cancer; male fertility; pancreatic disease.

XX OS Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US13360.

XX 27-APR-2000; 2000US-199963P.

PR 11-MAY-2000; 2000US-203336P.

PR 25-MAY-2000; 2000US-207087P.

PR 26-MAY-2000; 2000US-207546P.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;

PI Lai Y, Xie Q;

XX WPI: 2002-041392/05.

DR N-PSDB; ABA90354.

XX Novel polypeptides and polynucleotides useful as a vaccine for

preventing and treating diseases associated with the polypeptide, e.g.  
PT Alzheimer's disease, dyslipidemia, obesity, diabetes, infertility,  
PT asthma, amnesia

XX Claim 1; Page 100-101; 116pp; English.

PS The invention relates to an isolated polypeptide comprising a 277, 480,  
CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,  
CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,  
CC 784, 252, 592, 472, 607, 781, 640, 686 or 154 amino acid sequence as

given in the specification. The polypeptides, modulators of the  
CC polypeptides and antibodies against the polypeptides are useful for  
CC treating diseases such as neurological and psychiatric diseases  
CC including Alzheimer's, paraneuronal palsy, Huntington's disease,  
CC myotonic dystrophy, anorexia and depression; cardiovascular diseases  
CC including congestive heart failure, Hodgkin's disease and myocardial  
CC infarction; respiratory diseases including asthma, chronic obstructive  
CC pulmonary disease, cystic fibrosis and adult respiratory distress

syndrome; liver diseases including hypercholesterolaemia, cirrhosis,  
CC viral and nonviral hepatitis, Type II diabetes mellitus, and impaired  
CC glucose tolerance; renal disease including renal failure, acute tubular  
CC necrosis and glomerulonephritis; skeletal muscle diseases including  
CC Eulenburg's disease, hypoglycaemia and obesity; gastrointestinal  
CC diseases including myotonia congenita and intestinal obstruction; lymph  
CC diseases including lymphagietasia; diseases of placenta including  
CC choriocarcinoma; diseases of testes including testicular cancer,  
CC male reproductive diseases including low testosterone and male  
CC infertility; and disease of pancreas including diabetic ketoacidosis,  
CC Type 1 and 2 diabetes and obesity. The present sequence is a  
CC polypeptide of the invention.

XX Sequence 462 AA;

XX Query Match

Best Local Similarity 74.3%; Score 1878.5; DB 23; Length 462;

Matches 368; Conservative 15; Mismatches 66; Indels 31; Gaps 3;

1 MLGIWIVAFLEFGTSGRKYCYERLGCDFKGLPWTTRFTSTELVGLPWSPEKINTRFLLYT 60  
1 MLPLWTLIS-LLLGAAGVAGKEVCYERLGCDFSDSPWAGITERPHILPWSKDVNTRFLLYT 59  
61 IHNPNAYQEISAVNSSTIQASYFGTDKITRINIAGWKTGKQWDMCNVLLQLEDINCIN 120  
60 NENPNFQEISAVNSSTIQASYFGTDKITRINIAGWKTGKQWDMCNVLLQLEDINCIN 119  
121 LDWINGSREYIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180  
120 LDWINGSREYIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 179  
181 IPGLGRITGLDPAAGFFHNTPKVRLDPSDANFVDVHTNAARILFELGVGTIDACGHLD 240  
180 IPGLGRITGTHALQGLGECATEGYLSATLANNVFEVDN-----HMD 222  
241 FYPNGGKHMPGCCDLITPLL-----KFNFNAYKKEVASFFDCNHNARSQYFA 287  
223 ATPILPQWMTSGTSNPLPVTSSLCNLADLGSVSLVCLMPEMASFFDCNHNARSQYFA 282  
288 ESILNPDAFIAYPCRSYTSFKAGNCFKSCGECPTMGHFAFRHFNKMKTNKNGSHYFLNTG 347  
283 ESILNPDAFIAYPCRSYTSFKAGNCFKSCGECPTMGHFAFRHFNKMKTNKNGSHYFLNTG 342  
348 SLSPFARWRHKL SVKLSGSEVTGTVFLRVGGAGVKTGTFEFAIVSGKLBPGMTYTKLIDAD 407  
343 SLSPFARWRHKL SVKLSGSEVTGTVFLRVGGAGVKTGTFEFAIVSGKLBPGMTYTKLIDAD 402  
408 VNVGNITSVQFIWKXHLFEDSQNKLGAEMVINTSGKYGYKSTFCSDQIMGNPILONLKP 467  
403 VNVGNITSVQFIWKXHLFEDSQNKLGAEMVINTSGKYGYKSTFCSDQIMGNPILONLKP 462

.J 7  
7589  
ABB97589 standard; Protein; 276 AA.

ABB97589;

27-JUN-2002 (first entry)

Novel human protein SEQ ID NO: 857.

Human; antianaemic; vulnary; antiinflammatory; immunomodulator;  
antinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;  
neuroprotective; antiparkinsonian; protein therapy; ESI;  
expressed sequence tag.

Homo sapiens.

WO200222660-A2.

21-MAR-2002.

10-SEP-2001; 2001WO-US26015.

11-SEP-2000; 2000US-0659671.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
Xue AJ, Yang Y, Wehrman T, Drmanac RT;

WPI; 2002-292408/33.

N-PSDB; ABN32775.

An isolated polynucleotide for treating diseases associated with its  
encoded polypeptide such as cancer and multiple sclerosis -

Claim 20; SEQ ID NO 857; 509pp; English.

The present invention provides the protein and coding sequences of 444

CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat  
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions  
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC Parkinson's disease. The present sequence is a protein of the invention.  
CC  
XX  
SQ Sequence 276 AA;

Query Match 57.6%; Score 1456; DB 23; Length 276;

Best Local Similarity 100.0%; Pred. No. 4.1e-137;

Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWIVAFLEFGTSGRKYCYERLGCDFKGLPWTTRFTSTELVGLPWSPEKINTRFLLYT 60

Db 1 MLGIWIVAFLEFGTSGRKYCYERLGCDFKGLPWTTRFTSTELVGLPWSPEKINTRFLLYT 60

QY 61 IHNPNAYQEISAVNSSTIQASYFGTDKITRINIAGWKTGKQWDMCNVLLQLEDINCIN 120

Db 61 IHNPNAYQEISAVNSSTIQASYFGTDKITRINIAGWKTGKQWDMCNVLLQLEDINCIN 120

QY 121 LDWINGSREYIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180

Db 121 LDWINGSREYIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180

QY 181 IPGLGRITGLDPAAGFFHNTPKVRLDPSDANFVDVHTNAARILFELGVGTIDACGHLD 240

Db 181 IPGLGRITGLDPAAGFFHNTPKVRLDPSDANFVDVHTNAARILFELGVGTIDACGHLD 240

QY 241 FYPNGGKHMPGCCDLITPLLPFNAYKK 269

Db 241 FYPNGGKHMPGCCDLITPLLPFNAYKK 269

RESULT 8

ABB79040

ID ABB79040 standard; Protein; 469 AA.

XX

AC ABB79040;

DT 01-AUG-2002 (first entry)

XX Myocastor coypus pancreatic lipase related protein precursor SEQ:4.

DE Lipase; therapeutic; pancreatic lipase related protein precursor;

XX enzyme.

XX Myocastor coypus.

XX US2002052034-A1.

XX 02-MAY-2002.

XX 14-DEC-2000; 2000US-0735933.

XX 28-SEP-2000; 2000US-235925P.

XX (GUEG/) GUEGLER K.

XX (WEBS/) WEBSTER M.

XX (KETC/) KETCHUM K A.

XX (DFRA/) DI FRANCESCO V.

XX (BEAS/) BEASLEY E M.

XX Guegler K, Webster M, Ketchum KA, Di Francesco V, Beasley EM;

XX WPI; 2002-443697/47.

XX A lipase protein identified from the human genome is related to the  
XX pancreatic lipase subfamily, and is useful to provide new drug targets  
XX in the discovery of therapeutics for lipase-mediated disease -



Rat pancreatic lipase related protein precursor SEQ ID NO:6.

Lipase; therapeutic; pancreatic lipase related protein precursor; enzyme.

Rattus norvegicus.

US2002052034-A1.

02-MAY-2002.

14-DEC-2000; 2000US-0735933.

28-SEP-2000; 2000US-235925P.

(GUEG/) GUEGLER K.

(WEBB/) WEBSTER M.

(KETCH/) KETCHUM K A.

(DFRA/) DI FRANCESCO V.

(BEAS/) BEASLEY E M.

Guegler K, Webster M, Ketchum KA, Di Francesco V, Beasley EM;

WPI; 2002-443697/47.

A lipase protein identified from the human genome is related to the pancreatic lipase subfamily, and is useful to provide new drug targets in the discovery of therapeutics for lipase-mediated disease

Disclosure; Fig 2; 85pp; English.

The present invention describes a human lipase protein. Molecules from the present invention can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate lipase activity in cells and tissues that express lipase. The present sequence represents a pancreatic lipase related protein precursor isolated from rat, which is given in comparison with the human lipase in the exemplification of the present invention.

Sequence 467 AA;

Query Match 46.4%; Score 1172; DB 23; Length 467;  
 Best Local Similarity 49.3%; Pred. No. 2.8e-108;  
 Matches 232; Conservative 73; Mismatches 158; Indels 8; Gaps 6;  
 1 MLCIWTVAFLFFGTSRGKEVCYERLGCFCGDPWTRTFSTELVGLPWSPEKINTRELLYT 60  
 1 MTLTWVSLFILGAQGGKEVCYDNLCGSDPAEPWAGTAIRPLKLLPWSPEKINTRELLYT 60  
 61 IHNPNAYQEISAVNSSTIOASYFGTDKTRINIAGW--KTDGKQWQDMCNVLLQLEDINC 118  
 61 NENPTAFQTLQSLDPLTIGASNFQVARKTRTFIHGFDKGESWVDMCKMFQVEEVNC 120  
 119 INLDWINGSR-EYIHAVNNLRVVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177  
 121 ICVDWKKGSQATYTQANNRVVVGQAQVQMDILVKNYSYSPSKVHLIGHSLGAHLAGEA 180  
 178 GSRIPLGLGRITGLDPAGPFPHNTPKCEVRDPDSDANFVDVIHTNAARILFELGVGTIDACG 237  
 181 GSKTPGLSRITGLDPVEANFECTPEEVLDPDSDADFDVDVIHTDAAPLIFLFGTQMMSG 240  
 238 HLDVFNKGKHPGC-EDLIPLLFKNFNAYKEMASFFDCNHRARSQTFVAESILNPDAF 296  
 241 HLDVFNKGKHPGC-EDLIPLLFKNFNAYKEMASFFDCNHRARSQTFVAESILNPDAF 298  
 297 IAYPCRSYTSFKAGNCFKSCGECPTMGHFADRHFKNMKNMGSHYFLNTGSLSPPARWR 356  
 299 AAYPCASYKDPESNCFPCPDGCPQMGHYADKAGKS-GDEPKPFLNTGEAKNPARWR 357  
 357 HKLSVKLSGSEVTOQTVFLRVGGAIGKTEGFAIVSGKLEPQMTYTKLIDAVNVGNITSV 416  
 358 YRVSLILSGRMVT-QGVKVALFGSGKNTROYDIPRGIIKPGATHSSSEFDKLDVGTIEKV 416

QY 417 QFIWKHLFEDSQKLGAEWVINTSGKYGYKSTFCSDIMCPNILONLKPC 467  
 Db 417 KFLWNNQVINFSFKVGAAKITVQGBERTYFNCSBETVREDTLLTLIPC 467

RESULT 11

ABB06317  
 ID ABB06317 standard; Protein; 467 AA.

AC ABB06317;

DT 27-MAY-2002 (first entry)

DE Plrpl amino acid sequence.

KW Human; phospholipase A1; PLA1; enzyme; lipase; phosphatidic acid;  
 KW cytosolic; cellular regulation; transmembrane protein; cancer;  
 KW lipase regulation disorder.

OS Unidentified.

PN WO200202762-A1.

PD 10-JAN-2002.

PF 03-JUL-2000; 2000WO-JP04441.

PR 03-JUL-2000; 2000WO-JP04441.

PA (MOCH ) MOCHIDA PHARM CO LTD.

PI Inoue K, Arai H, Aoki J;

DR WPI; 2002-188424/24.

XX New human phospholipase PLA1 which specifically cleaves phosphatidic  
 PT acid, useful in the diagnosis, treatment and prevention of diseases  
 PT associated with lipase regulation disorders, including cancer -

PS Example; Fig 3; 68pp; Japanese.

XX The present invention describes human phospholipase A1 (PLA1) which  
 CC specifically cleaves phosphatidic acid (PA). PLA1 has cytosolic  
 CC activity. Phosphatidic acid is a messenger for cellular regulation  
 CC and the lipase is a transmembrane protein involved in its control.  
 CC PLA1 can be used in the diagnosis, treatment and prevention of  
 CC diseases associated with lipase regulation disorders, including cancer.  
 CC The present sequence represents an amino acid sequence given in  
 CC comparison with the human PLA1 amino acid sequence, in an example from  
 CC the present invention.

XX Sequence 467 AA;

Query Match 46.0%; Score 1162; DB 23; Length 467;  
 Best Local Similarity 48.6%; Pred. No. 2.8e-107;  
 Matches 229; Conservative 75; Mismatches 159; Indels 8; Gaps 6;

QY 1 MLCIWTVAFLFFGTSRGKEVCYERLGCFCGDPWTRTFSTELVGLPWSPEKINTRELLYT 50  
 Db 1 MLIWTITLFLGAQGGKEVCYEDLGCFSDEPWGTAIRPLKLLPWSPEKINTRELLYT 50

QY 61 IHNPNAYQEISAVNSSTIOASYFGTDKTRINIAGW--KTDGKQWQDMCNVLLQLEDINC 118  
 Db 61 NENPNFQILLSDPSSTIASNFQMDKTRTFIHGFDKGESWVDMCKLFEVEVNC 120

QY 119 INLDWINGSR-EYIHAVNNLRVVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177  
 Db 121 ICVDWKKGSQATYTQANNRVVVGQAQVQMDILVKNYSYSPSKVHLIGHSLGAHLAGEA 180

QY 178 GSRIPLGLGRITGLDPAGPFPHNTPKCEVRDPDSDANFVDVIHTNAARILFELGVGTIDACG 237  
 Db 181 GSKTPGLSRITGLDPVEANFECTPEEVLDPDSDADFDVDVIHTDAAPLIFLFGTQMMSG 240

238 HLDYFNGGKHPGC-EDLITPLKFNFNAYKEMASFFDCNHAESYQFYAESILNPDFA 296  
 241 HLDFFNGGSMPCGCKNALSQIV--DLDIGWAGTRDFVACNHLRSYKYLESLNPDGF 298  
 297 IAYPCRSYTSFKAGNCFKSGKGCPTMGHFAHFRHFKMKTNGSHYFLNTGSLSPFARWR 356  
 299 AAYPCSYKSFSDCKFCPCDQCGCPQMGHYADKFAGRTSBQ-QKFFLNTGEASNFARWR 357  
 357 HKLSVKLSGSEVTOGTFLRVGGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416  
 358 YGVSTILSGRTAT-GQIKVALFGNGNTHQVSIIFRGLKPGSTHSYFSDAKLDVGTIEKV 416  
 417 QFTWKHLFEDSQNKLGAEMVINTSGKYGKSTFCSQDIMGPNILQNKPC 467  
 417 KFLWNNVINPLPKVGATKITVQGEKTVNFCSEDTVEEDTLTLTPC 467

I 12

741

AAR30741 standard; Protein; 470 AA.

AAR30741;

25-MAR-2003 (updated)

20-MAY-1993 (first entry)

GPL(+) mutant with HPL loop structure.

Guinea Pig Pancreatic Lipase; GPL; mini-loop; Human; detergent;  
 cystic fibrosis; CF; chronic pancreatitis;  
 exocrine pancreatic insufficiency.

Cavia porcellus.

Key Location/Qualifiers  
 Region 258..280  
 /label= HPL loop  
 /note= "replaces GPL mini-loop"

MO9300426-A1.

07-JAN-1993.

25-JUN-1992; 92WO-DK00200.

25-JUN-1991; 91EP-0610056.

(NOVO ) NOVO-NORDISK AS.

Jormsen E, Hjorth SA, Thim L, Verger R, Woldike HF;

NPI; 1993-036374/04.

N-PSDB; AAQ35064.

Guinea pig and human pancreatic lipase(s) and variant(s) - used  
 in detergents or as digestive enzymes for patients with cystic  
 fibrosis and chronic pancreatitis

Claim 16; Page 49 and Page 38-40; 65pp; English.

The Guinea pig pancreatic lipase sequence shows a high degree of  
 homology to other mammalian pancreatic lipases except for a distinct  
 discrepancy in the central part of the gene. This region encompasses  
 the 23 amino acid "loop structure" of human pancreatic lipase which  
 is substituted by a 5 amino acid "mini-loop" in GPL (see AAR30737 and  
 AAR30738 for native GPL and HPL sequences, respectively). The  
 GPL(+) variant in which the GPL mini-loop is substituted by the  
 HPL loop is claimed. The variant coding sequence was synthesised by  
 PCR (see AAQ35035-Q35038). Sequence AAR30741 is a combination of the  
 appropriate regions of the human and guinea pig amino acid sequences  
 linked according to the description given in the specification.  
 (Updated on 25-MAR-2003 to correct FN field.)

XX  
 SQ Sequence 470 AA;  
 Query Match 45.9%; Score 1159; DB 14; Length 470;  
 Best Local Similarity 48.2%; Pred. No. 5.7e-107;  
 Matches 228; Conservative 67; Mismatches 168; Indels 10; Gaps 6;  
 QY 1 MLGIWIVAFLEFGTSRGKEVCYERLGCFLKDPWTRTFSTELVGLPWSPEKINTRFLLYT 60  
 Db 2 MLFAWTIGLLJLATVRGAECVYSHLGCFSDEKPWAGTSORPIKSLPSDPKINTRFLLYT 61  
 QY 61 IHNPNAYOEISAVNSSTIOASYFTQDKITRINIAGWTKDGK--WORDMCNVLLQLEDINC 118  
 Db 62 NENQNSYQLITATDIATIKAGNFNLKTRFIIHGFTDSGENSWLSDMKCNMFQVEKVCNC 121  
 QY 119 INLDWINGSR-EYTHAVNNLRVGAEVAYFDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177  
 Db 122 ICVDWKGSKAQYSCASQNRVVGAEVAYLVQVLSLNYAPENVHIIHSLGAHTAGEA 181  
 QY 178 GSRIPGL-GRITGLDPAGPPFHNTPKFVRLDPSDANFVDVIHTNAARILFELGVGTIDAC 236  
 Db 182 GKRLNGLVGRITGLDPAEPYFQDTPPEVRLDPSDAKEFVDVIHTDISPILPSLGFSGMSQV 241  
 QY 237 GHLDPYNGGKHPGCEDLITPLKFNFNAYKEMASFFDCNHAESYQFYAESILNPDFA 296  
 Db 242 GHMDFNGGKMPGCKNLSQI-VDIGIWGTRDFAACNHRHSIEYHSHSILNPEGF 300  
 QY 297 IAYPCRSYTSFKAGNCFKSGKGCPTMGHFAHFRHFKMKTNG--SHYFLNTGSLSPFAR 354  
 Db 301 LGYPCASYDFEQSGCFPCPAKGCPCWGHFADQY---PGKTNAVEQTFELNTGASDNFIR 357  
 QY 355 WEHKLKSVKLSGSEVTOGTFLRVGGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNGNIT 414  
 Db 358 WRYKVTYVTLGEXKDPGSGNIINVALIGKNGNSAQYQVFKGTLKPDASYTNSIDVELNVGTIQ 417  
 QY 415 SVQFIWKHLFEDSQNKLGAEMVINTSGKYGKSTFCSQDIMGPNILQNKPC 467  
 Db 418 KVTFLWKESGISVSKPKMGASRITVQSGKDGTKYNFCCSDIVQENVEQTLSPC 470

RESULT 13

AAR30737

ID AAR30737 standard; Protein; 452 AA.

AC AAR30737;

XX

DT 25-MAR-2003 (updated)

DT 20-MAY-1993 (first entry)

XX

DE Guinea pig pancreatic lipase.

XX

KW GPL detergent; cystic fibrosis; CF; chronic pancreatitis;  
 KW exocrine pancreatic insufficiency.

XX

OS Cavia porcellus.

XX

FH Key Location/Qualifiers

FT Peptide 1..18

FT /label= signal\_peptide

FT Protein 19..452

FT /label= GPL

FT Region 258..262

FT /label= mini-loop

FT /note= "central homology gap region, c.f. HPL"

XX MO9300426-A1.

XX

PD 07-JAN-1993.

XX

PF 25-JUN-1992; 92WO-DK00200.

XX

PR 25-JUN-1991; 91EP-0610056.

XX

(NOVO) NOVO-NORDISK AS.

Gormsen E, Hjorth SA, Thim L, Verger R, Woldike HP;

WPI; 1993-036374/04.  
N-PSDB; AAQ35058.

Guinea pig and human pancreatic lipase(s) and variant(s) - used in detergents or as digestive enzymes for patients with cystic fibrosis and chronic pancreatitis

Claim 1; Page 38-40; 65pp; English.

A cDNA library was constructed from mRNA isolated from homogenised guinea pig pancreas. The library was transformed into competent SC51 cells. Recombinant clones were transferred to nitrocellulose filters and probed with degenerate probe pools based on the amino acid sequences of peptide fragments from purified GPL (see AAQ35060 and AAQ35061). Four clones were positive to both probe pools and were selected as putative GPL clones. All four were confirmed as GPL cDNA clones by sequencing. The GPL sequence shows a high degree of homology to other mammalian pancreatic lipases except for a distinct discrepancy in the central part of the gene. This region encompasses the 23 amino acid "loop structure" of human pancreatic lipase which is substituted by a 5 amino acid "mini-loop" in GPL (see AAQ35059 for coding HPL sequence). GPL encoded by this cDNA sequence can be used in detergent compositions or to treat lipase deficiency. Also claimed are C-terminally truncated forms of GPL and variants carrying an insertional substitution, pref. of the HPL loop structure in place of the GPL mini-loop and/or substitution of Cys103 or Cys105, pref. by Ser or Thr and further by substitution of Ser154 by Thr and/or Asp178 by Glu.  
(Updated on 25-MAR-2003 to correct PN field.)

Sequence 452 AA;

Query Match 45.7%; Score 1156; DB 14; Length 452;  
Best Local Similarity 48.0%; Pred. No. 1.1e-106;  
Matches 22; Conservative 64; Mismatches 154; Indels 28; Gaps 6;  
1 MLCIIVAFVFFGTSRGEVYERLCGKDFGTPWTFSTELVGLPWSPEKINTRFLYYT 60  
2 MLFAWTIGLLLATVRGAECYVSHLGCPSDEXPWAGTSORPIKSLPSPDKINTRFLYYT 61  
61 IHNPNAYQISAVNSSTIOASYGTGKTRIMAGKTDGK--WORDMNVLLQLEDINC 118  
62 NENQNSYQLTATDIATIKASNFNLMRKTRFIHGTDSGENSLSDMKMFMQVEKYNVC 121  
119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKPEYSPSKVHLGHSLGAHLAGEA 177  
122 ICVDWKGSQAQYSQASQIRVVGAEVAVLVQVLSLNYAPENVHIGHSIGAHTAGEA 181  
178 GSRIPGL-GRITGLDPAGFFHTPKVEVRLDPSDANFVDTNARILFELGVGTIDAC 236  
182 GKRLNGLVGRITGLDPAEPYFQDTPVEVRLDPSDAKFDVVIHDTSPILSLFGMSQKV 241  
237 GHLDYFNKGKHPGGEDLITPLKFNFNAYKEMASFFDCNHARSYOFYAESILNPDAP 296  
242 GHWDFFNKGKHPGGCKTGIS-----CNHRSIERYHSSILNPGPF 282  
297 IATPCRSYTFKAGNCFPCKGCEPTMGHFAHFPHKMKNTNG--SHYFLNTGSLSPPAR 354  
283 LGYPCASYDFQBSGCFPCPAKGCPRMGHFAQY---PGKTNAVEQTFFLATGASDNFTR 339  
355 WRHKLVSKLSSGVTOCTVFLRVGGAIGTGBEALVSGKLEFGMYTKLIDADVNGNIT 414  
340 WRKYVTVLSGKDPGSGNINVALLGKNGNSAQVQFKGLTKFDASYTNSIDVELNVTIQ 399  
415 SVQFIWKHLFEDSQNKLGAEMVINTSGKYGYKSTFCSDQINGPNILQKRPC 467  
400 KVTFLMKRSIGSVKPKMGASRITVQSGKDGTKYNPCSSDIQVENVQTLSPC 452

RESULT 14

ABG16896  
ID ABG16896 standard; Protein; 469 AA.  
XX  
AC ABG16896;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #16887.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US08631.  
PF 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS81083.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -  
PT  
PT  
PT  
XX  
XX Claim 20; SEQ ID No 47255; 103pp; English.  
PS  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.  
XX Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ  
Sequence 469 AA;  
Query Match 45.6%; Score 1152; DB 22; Length 469;  
Best Local Similarity 47.8%; Pred. No. 2.9e-106;  
Matches 225; Conservative 68; Mismatches 172; Indels 6; Gaps 5;  
QY 1 MLCIIVAFVFFGTSRGEVYERLCGKDFGTPWTFSTELVGLPWSPEKINTRFLYYT 60  
DB 1 MLFPWTIGLLLATVRGAECYVSHLGCPSDEXPWAGTSORPIKSLPSPDKINTRFLYYT 60  
QY 61 IHNPNAYQISAVNSSTIOASYGTGKTRIMAGKTDGK--WORDMNVLLQLEDINC 118  
DB 61 NENQNSYQLTATDIATIKASNFNLMRKTRFIHGTDSGENSLSDMKMFMQVEKYNVC 120



GenCore version 5.1.6  
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protein - protein search, using sw model

January 6, 2004, 11:12:33 ; Search time 28 Seconds  
(without alignments)  
1603.956 Million cell updates/sec

US-10-038-517-2  
t score: 2527  
ce: 1 MLGWIWVAFLEFCTSRGKEV.....STFCSQDIMGPNILQNLKPC 467

g table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ed: 283308 seqs, 96168682 residues

number of hits satisfying chosen parameters: 283308

m DB seq length: 0

m DB seq length: 2000000000

rocessing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

se : PIR.761\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Score	Query Match	Length	DB ID	Description
1191	47.1	470	2 A54232	lipase, CoPL-RP2 -
1174	46.5	467	1 LIDG	triacylglycerol li
1172	46.4	473	2 S20612	triacylglycerol li
1162	46.0	467	2 A43357	pancreatic lipase-
1152	45.6	469	2 B43357	pancreatic lipase-
1147.5	45.4	457	2 A48206	triacylglycerol li
1142.5	45.2	482	1 A46696	triacylglycerol li
1129.5	44.7	482	1 A34571	triacylglycerol li
1121	44.4	434	1 A49488	triacylglycerol li
1115	44.1	465	2 C43357	triacylglycerol li
1109	43.9	461	2 S21223	triacylglycerol li
1108	43.8	465	1 S41064	triacylglycerol li
1107	43.8	465	1 JC1318	triacylglycerol li
1039.5	41.1	449	1 LIPG	triacylglycerol li
534	21.1	499	2 A28997	triacylglycerol li
503	19.9	510	2 S15893	triacylglycerol li
483	19.1	494	2 A27442	triacylglycerol li
471	18.6	465	1 A27330	lipoprotein lipase
459	18.2	478	2 S18158	lipoprotein lipase
458.5	18.1	490	1 S04331	lipoprotein lipase
453	17.9	475	1 LTHUL	lipoprotein lipase
452	17.9	478	2 S29846	lipoprotein lipase
450	17.8	475	2 JC4242	lipoprotein lipase
445.5	17.6	474	1 JH0790	lipoprotein lipase
444.5	17.6	450	1 A27053	lipoprotein lipase
442.5	17.5	474	1 A40570	lipoprotein lipase
318.5	12.6	172	2 A45658	triacylglycerol li
287	11.4	303	2 A44563	phospholipase A1
284.5	11.3	300	2 A44564	phospholipase A1

RESULT 1

A54232  
lipase, CoPL-RP2 - nutria  
C:Species: Myocastor coypus (nutria, coypu)  
C:Date: 22-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Feb-1997  
C:Accession: A54232  
R:Thirstrup, K.; Verger, R.; Carriere, P.  
Biochemistry 33, 2748-2756, 1994  
A:Title: Evidence for a pancreatic lipase subfamily with new kinetic properties.  
A:Reference number: A54232; PMID:94176463; PMID:9130186  
A:Accession: A54232  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-470 <THI>  
A:Experimental source: pancreas  
A:Note: sequence extracted from NCBI backbone (NCBIP:144530)  
C:Superfamily: triacylglycerol lipase

Query Match	47.1%;	Score 1191;	DB 2;	Length 470;
Best Local Similarity	49.8%;	Pred. No. 2.5e-88;		
Matches 236;	Conservative 63;	Mismatches 163;	Indels 12;	Gaps 7;
Qy	1	MLGIWIVAFLEFCTSRGKEVYERLGCPCFKDGLPWRTRTFSTBLVGLPWPSPKINTRFLLYT	60	
Db	2	MLFVWTTGLLLATARGNEVCYSHLGCFSDEKPMAGTLQRPVKSILPASPEINTRFLLYT	61	
Qy	61	IHNPNAYQISAVNSSTTQASYPGTDKJTRINIAWKTDGK--WORDMNVLLQLEDINC	118	
Db	62	NENPNYQITATDPATIKASFNLRKTRFVHGFIDNGEKDLTDICKRMFQVEKVC	121	
Qy	119	INLDWINGRE-YIHAVNNLRVVGAEVAVFDVLMKPEYSPSKVHLIGHSLGAHAGEA	177	
Db	122	ICVDWOGGSLATYSAQVQNIIVVGAEVAVLVQVLSDLQGYKPGNVHMLGHSLGAHTAAEA	181	
Qy	178	GSRIPL-GRITGLDPAGFFHNTPKVRLPDSANFVDVIHTNAARILFELGVGTIDAC	236	
Db	182	GRRLKLVGRITGLDPAPPCFQDTPPEVRLPDSANFVDVIHTDIAPISFGFGMSQKV	241	
Qy	237	GHLDYFVPGKHKMPGCE-DLITPLKPNFNAYKXEMASFFPDONHARSYQFYAESLTPDA	295	
Db	242	GHMDFPFGKHKMPGCKNIIITIV--DVNGFLEGITLAAACNHNRSYQYSSSLTPPDG	299	
Qy	296	FIAYPCRSYTSFKAGNCFFCSKEGCPTMGHFAFRPHFKNMKTNG--SHYFLNTGSLSPFA	353	
Db	300	FLGYPCASYEEFKDGCPCPAEGCPCPKGHVADQF--QGKANGVEKTYFLNTGSDSNFP	356	
Qy	354	RWRHKLKVLKSSSEVTQGTVFRVCGAIGKYGFAIVSGKLEPGMTYTKLIDADVNCNI	413	
Db	357	RWRKYKSVTLSEKLSGDIKIALFGRNGSKQVIFKGSILKPDARYTHDIDVNLNGEI	416	
Qy	414	TSVQFTWKHLPEDSONKLGASWINTSGKYGKSTFCSDQDMGNILQNLKPC	467	

phospholipase A1 -  
vitellogenin I pre  
yolk protein 2 - b  
yolk protein 3 - b  
vitellogenin III p  
vitellogenin II pr  
vitellogenin 2 - M  
vitellogenin 1 - M  
probable thioester  
hypothetical 303aa  
hypothetical prote  
alpha-amylase (EC  
alpha-amylase (EC  
apolipoprotein B -  
UV-damaged DNA-bin  
phosphopyruvate hy



417 QKVKFLWHNNINLLOPKLGASQITVQSGEYGTQYKFNCSNNTVQSDVLQSLSPC 470

T 2

ylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - dog  
ernate names: triacylglycerol acylhydrolase  
ies: Canis lupus familiaris (dog)  
e: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 31-Mar-2000  
ession: B24392; A32615; E30034  
felec, B.; LaForge, K.S.; Puigserver, A.; Scheele, G.  
eas 1, 430-437, 1986  
le: Primary structures of canine pancreatic lipase and phospholipase A2 messenger R  
erence number: A93751; MUID:87175472; PMID:3562437  
ession: B24392

ecule type: mRNA  
idues: 1-467 <ER>  
ss-references: GB:M35302; NID:g164047; PIDN:AAA30885.1; PID:g164048  
e: the authors translated the codon UGC for residue 21 as Lys  
kel, F.S.; Weidenbach, F.; Swatovsky, B.; LaForge, K.S.; Scheele, G.A.  
O.L. Chem. 284, 12895-12901, 1989  
le: Structure of the canine pancreatic lipase gene.  
erence number: A32615; MUID:89327249; PMID:2502543  
ession: A32615  
ecule type: DNA  
idues: 1-91, 1, 93-97, 'D', 99-264, 'D', 266-467 <MIC>  
eics:

rons: 17/1; 68/3; 110/3; 155/3; 192/1; 232/1; 272/1; 311/3; 355/1; 391/2; 447/2

erfamily: triacylglycerol lipase  
ords: carboxylic ester hydrolase; lipid digestion; pancreas  
7/Domain: signal sequence #status predicted <SIG>  
467/Product: triacylglycerol lipase, pancreatic #status predicted <MPT>  
194,281/Active site: Ser, Asp, His #status predicted

ry Match 46.5%; Score 1174; DB 1; Length 467;

t Local Similarity 48.2%; Pred. No. 5.8e-87;  
ches 227; Conservative 78; Mismatches 158; Indels 8; Gaps 6;

1 MLGIWIVAFPGTSRGKVCYERLGCFCGKGLPWTRTFSTELVGLPWSPEKINRFLLYT 60

1 MWSIWTIALFLGAARKEVCYEQIGCFSDAEPWAGTAIRPLKVLPSPEKIGRFLLYT 60

61 IHNPAYQISAVNSTIOASYFGTDKITRINIAGW--KTDGKQWDMCNVLLQLEDINC 118

61 NKPNNFQTLPSDPTIEASNFQDKKTRFTIHGFINKGEENWVDMCKMFKVEVNC 120

119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKFEYSPSKVHLIGHSLGAHLAGEA 177

121 ICVDWKGSQTSYTOAANNRVVGAQVACLMSLSANSYSFSPQVQLIGHSLGAHVAGEA 180

178 GSRTPGLGRITGLDPAGPPFHTPKEVRLDPSDANFVDVHTNAARILFELGVGTIDACG 237

181 GSRTPLGLGRITGLDPVEASFQGTPEVRLDPTDADFVDVHTDAAPLIPFLGFTSQMG 240

238 HLDYPNGGKHPGC-EDLITPLLKFNAYKEMASFFDCNHARSYQFYAESILNPDFAF 296

241 HLDFFPNGGEPMGCKKXALSQIV--NLDGIWEGTRDFVACNHLRSYKYSESLINDPGF 298

297 IAYPCRSYTSFKAGNCFKSCGCGCTMGHEADRHFKNMKTNGSHYFLNTGSLSPFARWR 356

299 ASVPCASYRAFESNCKFCPCDQCGCPQMGHYADKFAVKT-SDETOKYFLNTGSDSNFARWR 357

357 HKLSVKLSGSEVTQGTFLRVGGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416

358 YGVSIITLSGKRAT-GQAKVALFGSKGNTHQFNIPKGLKPGSTHSEFADKLDVGTIEKV 416

417 QFTWKKHLFEDSQNKLGAEMVINTSGKYGYKSTFCSDIMGNPILQNLKPC 467

417 KFLMNNVNPFPFKVGAAKITVQKGEERTYFNFCSESTVREDVLLTLTPC 467

T 3

2

triacylglycerol lipase (EC 3.1.1.3) precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 18-Jun-1999  
C:Accession: S20612

R;Wicker-Planquart, C.; Puigserver, A.  
FEBS Lett. 296, 61-66, 1992

A:Title: Primary structure of rat pancreatic lipase mRNA.  
A:Reference number: S20612; MUID:92111786; PMID:1730292

A:Accession: S20612

A:Molecule type: mRNA

A:Residues: 1-473 <MIC>

A:Cross-references: EMBL:X61925; NID:956599; PIDN:CAA43927.1; PID:956600

C:Superfamily: triacylglycerol lipase

C:Keywords: carboxylic ester hydrolase

Query Match 46.4%; Score 1172; DB 2; Length 473;

Best Local Similarity 49.3%; Pred. No. 8.5e-87;  
Matches 232; Conservative 73; Mismatches 158; Indels 8; Gaps 6;

QY 1 MLGIWIVAFPGTSRGKVCYERLGCFCGKGLPWTRTFSTELVGLPWSPEKINRFLLYT 60

Db 1 MLTLWTVSLFLLGAAQKQKVCYDNLGCFSDAEPWAGTAIRPLKLLPWSPEKINRFLLYT 60

QY 61 IHNPAYQISAVNSTIOASYFGTDKITRINIAGW--KTDGKQWDMCNVLLQLEDINC 118

Db 61 NENPTAFQTLQSLDPLTIGASNFQVARKTRFIHGFIDKGEENWVDMCKMFKVEVNC 120

QY 119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKFEYSPSKVHLIGHSLGAHLAGEA 177

Db 121 ICVDWKGSQTSYTOAANNRVVGAQVACLMSLSANSYSFSPKVLIGHSLGAHVAGEA 180

QY 178 GSRTPGLGRITGLDPAGPPFHTPKEVRLDPSDANFVDVHTNAARILFELGVGTIDACG 237

Db 181 GSRTPLGLGRITGLDPVEANFEGTPEEVRFLDPSDADFVDVHTDAAPLIPFLGFTNQMSG 240

QY 238 HLDYPNGGKHPGC-EDLITPLLKFNAYKEMASFFDCNHARSYQFYAESILNPDFAF 296

Db 241 HLDFFPNGGQSWPCKKXALSQIV--DIDGIWSTDRDFVACNHLRSYKYSESLINDPGF 298

QY 297 IAYPCRSYTSFKAGNCFKSCGCGCTMGHEADRHFKNMKTNGSHYFLNTGSLSPFARWR 356

Db 299 AAYPCASYKDFESNCKFCPCDQCGCPQMGHYADKFAKGS-GDEPQKFPFLNTGEAKNFARWR 357

QY 357 HKLSVKLSGSEVTQGTFLRVGGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416

Db 358 YRVSILISGRNVT-GQKVALFGSKGNTRQIDIFRGLIKPGATHSSSEFADKLDVGTIEKV 416

QY 417 QFTWKKHLFEDSQNKLGAEMVINTSGKYGYKSTFCSDIMGNPILQNLKPC 467

Db 417 KFLMNNVNPFPFKVGAAKITVQKGEERTYFNFCSESTVREDVLLTLTPC 467

RESULT 4

A43357

pancreatic lipase-related protein 1 precursor - human

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Mar-2000

C:Accession: A43357

R;Gillier, T.; Buchwald, P.; Blum-Kaelin, D.; Hunziker, W.

J. Biol. Chem. 267, 18509-18516, 1992

A:Title: Two novel human pancreatic lipase related proteins, hLURP1 and hLURP2. Different

A:Reference number: A43357; MUID:92355622; PMID:1379598

A:Accession: A43357

A:Molecule type: mRNA

A:Residues: 1-467 <GIL>

A:Cross-references: GB:M93283; NID:g187229; PIDN:AAA59532.1; PID:g187230

A:Note: sequence extracted from NCBI backbone (NCBIN:110821, NCBIPI:110822)

C:Genetics:

A:Gene: GDB:PLNLRP1; PLNRP1

A:Cross-references: GDB:I34816

C:Superfamily: triacylglycerol lipase

F.1-17/Domain: signal sequence #status predicted <SIG>

F.18-467/Product: pancreatic lipase-related protein 1 #status predicted <MAT>

cy Match 46.0%; Score 1162; DB 2; Length 467;  
 Local Similarity 48.8%; Pred. No. 5.4e-86;  
 ches 229; Conservative 75; Mismatches 159; Indels 8; Gaps 6;  
 1 MLGIWIVAFLLFGTSRGKVCYERLGCFCGDLGTPWTRTFSTELVGLPWSPEKINTRELLYT 60  
 1 MLIFWITLFLGAAKKEVCYEDLGCSTDEPGWGTARLKLPLPWSPEKIGTRFLLYT 60  
 61 IHNPNAYQISAVNSSTIOASVFGTDKTRINIAW--KTDGKQWDMCNVLLQLEDINC 118  
 61 NENPNFQILLSDPSTIEASNFQMDRTRFIHGFIDKGDSEWVTDCKLFEVEVNC 120  
 119 INLDWNGSR-EYHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHAGEA 177  
 121 ICVDWKKGSQAYTOANNRVVVGAAQMLDILTEYSYPPSKVHLIGHSLGAHAGEA 180  
 178 GSRIPGLRITGLDPAGPPFHTNPKVEALDPSDANFVDVHTNAARILFELGVGTIDACG 237  
 181 GSKTPGLSRITGLDPVEASFESTPEVRLDPSDADFVDVHTDAAPLIPFLGFTNQMG 240  
 238 HLDVYPNGKHMFGC-EDLITPLKFNFNAYKEMASFFDCNHARSQFYAESILNPDAP 296  
 241 HLDFFPNGSGMPGCKKXALSOIV--DLDGWAGTRDFVACNHLRSYKYLESLNPDGF 298  
 297 IAYPCRSYTSFKAGNCFPCSKGCGTGMGHFADRFHFNKMTNGSHYFLNTGSLSPPARWR 356  
 299 AAYPCTSYKSFSDKCFPCPDGCGQMGHYADKAGRTSEQ-QKFLNTGEASNFARWR 357  
 357 HKLSVKLSGSEVTQGVFLRVGAGIKGTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416  
 358 YGVSTLSGRAT-QGIKVALFGNKNTHOYSIFRGLKPGSTHSYEFDAKLDVGTIEK 416  
 417 QRIWKXHLFEDSONKLGAEWINTSGKYKSTFCSODIMGPNILQNLKPC 467  
 417 KLMNNVNPFLPVGATKITVQGEKTVNFCSEDTVREDTLLTLTPC 467  
 5  
 satic lipase-related protein 2 precursor - human  
 es: Homo sapiens (man)  
 a: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Mar-2000  
 sion: B43357  
 ler, T.; Buchwald, P.; Blum-Kaelin, D.; Hunziker, W.  
 l. Chem. 267, 16509-16516, 1992  
 le: Two novel human pancreatic lipase related proteins, hLPR1 and hLPR2. Differ-  
 erence number: A43357; MUID:92355622; PMID:1379598  
 sion: B43357  
 acule type: mRNA  
 lues: 1-469 <GIL>  
 as-references: GB:M93284; NID:g187231; PIDN:AAAS9533.1; PID:g187232  
 a: sequence extracted from NCBI backbone (NCBIN:110824, NCBIP:110825)  
 atics:  
 as-references: PLRP2  
 rfamily: triacylglycerol lipase  
 167/Product: pancreatic lipase-related protein 2 #status predicted <MAT>  
 cy Match 45.6%; Score 1152; DB 2; Length 469;  
 Local Similarity 47.8%; Pred. No. 3.5e-85;  
 ches 225; Conservative 68; Mismatches 172; Indels 6; Gaps 5;  
 1 MLGIWIVAFLLFGTSRGKVCYERLGCFCGDLGTPWTRTFSTELVGLPWSPEKINTRELLYT 60  
 1 MLPPWTLLGLLAVRGKVCYGLGCFSDKPKWAGTLQRPVKLLPWSPEKIDITRELLYT 60  
 61 IHNPNAYQISAVNSSTIOASVFGTDKTRINIAW--KTDGKQWDMCNVLLQLEDINC 118  
 61 NENPNFQILLTGTEDTIEASNFOLDKTRTRFIHGFIDKAEWSDMKCKMFEVEKVC 120  
 119 INLDWNGSR-EYHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHAGEA 177

Db 121 ICVDWRHGSRAMYTQAVQNIWVGAEATFLIQAALSTOLGYSLEDDVHVHIGSLGAHTAAEA 180  
 QY 178 GSRIPG-LGRITGLDPAGPPFHTNPKVEALDPSDANFVDVHTNAARILFELGVGTIDAC 236  
 Db 181 GRLGRVGRITGLDPAGCFQDPEEVRVLDPSDAVFDVHTDSSPIVPSLGFMSQKV 240  
 QY 237 GHLDFYPNGKHMFGCEDLITPLKFNFNAYKEMASFFDCNHARSQFYAESILNPDAP 296  
 Db 241 GHLDFPFGGKEMPGCKKNVLSTIT-DIDGIWEGIGGFVSCNHLRSFEYSSVNLNPDGF 299  
 QY 297 IAYPCRSYTSFKAGNCFPCSKGCGTGMGHFADRFHFNKMTNGSHYFLNTGSLSPPARWR 356  
 Db 300 LGYPCASVDEFQESKCFPCPAEGCPKMGHYADQFKGXTSAVEQT-FFELNTGESGNFTSWR 358  
 QY 357 HKLSVKLSGSEVTQGVFLRVGAGIKGTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416  
 Db 359 YKVSVTLSGKVKNGYIRIALYGSNENSKQYIEFKGSLKPDASHTCAIDVDVFNVGKLOKV 418  
 QY 417 QRIWKXHLFEDSONKLGAEWINTSGKYKSTFCSODIMGPNILQNLKPC 467  
 Db 419 KFLMNKRGINLSEPKLGASQITVQSGEDGTEYNFCSSDITVEENVLQSLYPC 469  
 RESULT 6  
 I48206  
 triacylglycerol lipase (EC 3.1.1.3) - nutria (fragment)  
 C:Species: Myocastor coypus (nutria, coypu)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
 C:Accession: I48206  
 R:Thiistrup, K.; Carriere, F.; Hjorth, S.A.; Raamussen, P.B.; Ladefoged, C.  
 Eur. J. Biochem. 227, 186-193, 1995  
 A:Title: Cloning and expression in insect cells of two pancreatic lipases and a procolip:  
 A:Reference number: I48204; MUID:95154288; PMID:7851384  
 A:Accession: I48206  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: mRNA  
 A:Residues: 1-457 <RBS>  
 A:Cross-references: EMBL:X82999; NID:g599870; PIDN:CAA58120.1; PID:g599871  
 C:Superfamily: triacylglycerol lipase  
 C:Keywords: carboxylic ester hydrolase  
 Query Match 45.4%; Score 1147.5; DB 2; Length 457;  
 Best Local Similarity 49.9%; Pred. No. 7.8e-85;  
 Matches 232; Conservative 69; Mismatches 149; Indels 15; Gaps 10;  
 QY 10 LFGTSRGKVCYERLGCFCGDLGTPWTRTFSTELVGLPWSPEKINTRELLYTINPNAYOE 69  
 Db 1 LLLGAVAGSEVCDRLGCFSDSPWAGIVERPLKLVFWSPTINTRELLYTINPNAYOI 60  
 QY 70 ISAVNSSTIOASVFGTDKTRINIAW--KTDGKQWDMCNVLLQLEDINCINLDWINGS 127  
 Db 61 VTA-DSSTIRSSNFRDTRKTRFIHGYIDKGNWLANMCEALLQVESVNCICVDWKGS 119  
 QY 128 RE-YIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHAGEASRIPG-LG 185  
 Db 120 RALYQATQNIWVGAEVAFVFDALQSLGSPSNVHIIHSLGSHVAGEAGRTNGNIG 179  
 QY 186 RITGLDPAGPPFHTNPKVEALDPSDANFVDVHTNAARILFELGVGTIDACGHLDFPNG 245  
 Db 180 RITGLDPAGPPFHTNPKVEALDPSDANFVDVHTDAGAPIPNLGFMSQTVGHLDFFPNG 239  
 QY 246 GKMPGCE-DLITPLKFNFNAYKEMASFFDCNHARSQFYAESILNPDAPAIYPCRSY 304  
 Db 240 GVEMPGQKNIISQIV--DINGIWEGRDFAACNHLRSYKYVIDSLNLTGTFAGFSCSY 297  
 QY 305 TSKAGNCFPCSKGCGTGMGHFADRFHFNKMTNG--SHYFLNTGSLSPPARWRHKLKSVK 362  
 Db 298 NTFSSNNCFPCASGCGPQMGHYADRF--SGKTNELFOQFYFLNTGDASNFSRWYQIAVT 354  
 QY 363 LSGSEVTQGVFLRVGAGIKGTGEFAIVSGKLEPGMTYTKLIDADVNGNITSVQFIWKK 422  
 Db 355 LSGRKVT-GHVLVSLVSGSGTQKQYIEYKSLQPGTSYVQIDSDVDVGDIEKVFIIWN 413



ry Match 44.4%; Score 1121; DB 1; Length 434;  
 t Local Similarity 48.4%; Pred. No. 1e-82;  
 ches 220; Conservative 63; Mismatches 144; Indels 28; Gaps 6;  
 19 EVCYERLGGKGLPWATFTSTFELVGLPWSPEKINTRELLYTHINPNAYQEIISAVNSSTI 78  
 2 EVCYHLGCFSDKPKWAGTSORPKSLSPDKKINTRELLYTNENQNSYQLITATDIATI 61  
 79 QASYFTGDKITRINIAWKTDGK--WORDMGNVLLQLEDINCINLMDWINGSR-EYIHAVN 135  
 62 KASNFNLNKRFTFIHGTDSGNSWLSDMKNMFQVEKVCNVCVDWKGSKQAYSOASQ 121  
 136 NRVVGAEVAYFIDVLMKKFYSKVKHLGHSIAGHLAGSAGSRIPGL-GRITGLDPAG 194  
 122 NRVVGAEVAYLVQVLSLTPNAPENVHIIHSHLCAHTAGAGKRLNGLVGRITGLDPAE 181  
 195 PFPHNTPEVRLLPDSANFVDVHTNAARILFELGVGTIDACGHLDFYPNGGKHEMCCED 254  
 182 PFQDTPEVRLLPDSAKFVDVHTDISPLPSLGFQMSQKVGHNDFPFGKMDPGCKT 241  
 255 LITPLKFNFNAYKEMASFFDCNHARSYQFYAESILNPDATFAYPCRSYTSFKAGNCFF 314  
 242 GIS-----CNHRSIEYHSSILNPEGLGYPCASYDFEQSGCFF 282  
 315 CSKGCPTMGHFAFRPHFNKNTNG--SHYFELNTGSLSPFARMHKLKSVKLSGEVTOGT 372  
 283 CPKAGCPKQKHGFADQY---PGKNAVEQTFELNGASDNFTRRYKVTYVTLSEKDPGSGN 339  
 373 VFLRVGGAIGTGEPAIVSGKLEPQNTYKLIADVNAGNITSVQFTKXKHLFEDSONKL 432  
 340 INVALLGXNGNSAQVQVFKGLTKDPASVTSIDVELNAGVLIQKTFELKSGSISVSKPKM 399  
 433 GAEMVINTSGKYGKYSTPCSDODINGPNILQNLKPC 467  
 400 CASRTVQSGKDGTKYCNFCSSDIVQENVEQTLSPC 434  
 1-glycerol lipase (EC 3.1.1.3) precursor, pancreatic - human  
 1-ate names: fatty acid ethyl ester synthase; pancreatic lipase  
 1-ies: Homo sapiens (man)  
 1-30-Sep-1993 #sequence revision 30-Sep-1993 #text change 31-Mar-2000  
 1-ssion: C43357; A34494; S08272; A60135; S34578; A34574  
 1-er: T.; Buchwald, P.; Blum-Kaelin, D.; Hunziker, W.  
 1-1. Chem. 267, 16509-16516, 1992  
 1-e: Two novel human pancreatic lipase related proteins, hPLRP1 and hPLRP2. Differ-  
 1-erence number: A43357; MUID:92355622; PMID:1379598  
 1-ssion: C43357  
 1-us: nucleic acid sequence not shown; translation not shown  
 1-ucle type: mRNA  
 1-ides: 1-465 <GIL>  
 1-s-References: GB:M93285; NID:G190139; PIDN:AAA60129.1; PID:G190140  
 1-ler, F.K.; Rosenblum, J.L.; Strauss, A.W.  
 1-1. Chem. 264, 20042-20048, 1989  
 1-le: Cloning and characterization of human pancreatic lipase cDNA.  
 1-erence number: A34494; MUID:90062115; PMID:2479644  
 1-ssion: A34494  
 1-ucle type: mRNA  
 1-ides: 1-465 <LOW>  
 1-s-References: GB:J05125; NID:G339596; PIDN:AAA36740.1; PID:G339597  
 1-ler, F.K.; D'Arcy, A.; Hunziker, W.  
 1-343, 771-774, 1990  
 1-le: Structure of human pancreatic lipase.  
 1-erence number: S08272; MUID:90158621; PMID:2106079  
 1-ssion: S08272  
 1-us: not compared with conceptual translation  
 1-ucle type: mRNA  
 1-ides: 17-46/48-465 <WIN>  
 1-3: part of this sequence, including the amino end of the mature protein, was confir-  
 1-aro, A.; Bonicel, J.; Pieron, G.; Guy, O.  
 1-mie 63, 799-801, 1981

A>Title: Comparative studies of human and porcine pancreatic lipases: N-terminal sequence  
 A'Reference number: A60135; MUID:82069208; PMID:7306587  
 A'Accession: A60135  
 A'Molecule type: protein  
 A'Residuals: 17-30, 'X', 32-33, 'X', 35-36, 'IOX', 40-41, 'X', 43-45 <DEC>  
 R.Thirstrup, K.; Carriere, F.; Hjorth, S.; Rasmussen, P.B.; Woeldike, H.; Nielsen, P.F.;  
 FEBS Lett. 327, 79-84, 1993  
 A>Title: One-step purification and characterization of human pancreatic lipase expressed  
 A'Reference number: S34578; MUID:93327921; PMID:8335100  
 A'Accession: S34578  
 A'Status: preliminary  
 A'Molecule type: protein  
 A'Residuals: 17-31 <THR>  
 R.Riley, D.J.S.; Kyger, E.M.; Spillburg, C.A.; Lange, L.G.  
 Biochemistry 29, 3848-3852, 1990  
 A>Title: Pancreatic cholesterol esterases. Purification and characterization of human par-  
 A'Reference number: A34574; MUID:90283377; PMID:2354155  
 A'Accession: A34574  
 A'Molecule type: protein  
 A'Residuals: 'X', 18-36 <RI>  
 A'Experimental source: pancreas  
 C:Genetics:  
 A'Gene: GDB:PNLIP  
 A'Cross-references: GDB:127916; OMIM:246600  
 A'Map position: 10q24-10q26  
 C:Superfamily: triacylglycerol lipase  
 C:Keywords: carboxylic ester hydrolase  
 F:1-16/Domain: signal sequence #status predicted <SIG>  
 F:17-465/Product: triacylglycerol lipase #status experimental <MAT>  
 Query Match 44.1%; Score 1115; DB 2; Length 465;  
 Best Local Similarity 47.8%; Pred. No. 3.4e-82;  
 Matches 226; Conservative 73; Mismatches 160; Indels 14; Gaps 10;  
 QY 1 MLGIWVAFLLPFGTSRGKVCYERLGCDFKGLPWTFTSTFELVGLPWSPEKINTRELLY 60  
 DB 1 MLPLWTLIS-LLLGA VAGKVCYERLGCDFSDSPSWSGITERPLHILPWSPKDVTNRELLY 59  
 QY 61 IHNPNAYQEIISAVNSSTIQASYFGTKITRINIAAG--KTDGKQSDMGNVLLQLEDINC 118  
 DB 60 NENPNFQEVAA--DSSSISGNSFKTNKTRFTIHFIDKGEENWLANVCNLFKVESVNC 118  
 QY 119 INLDWINGSRE-VIHAVNLRVVGAEVAYFIDVLMKKFYSKVKHLGHSIAGHLAGEA 177  
 DB 119 ICVDWKGSGSTGTQASQNIIRIVGAEVAYFVFLQSAFGYSNVEVIGHSIAGHLAGEA 178  
 QY 178 GSRIIPG-LGRITGLDPAGPPFHTPTKEVRLDPSDANFVDVHTNAARILFELGVGTIDAC 236  
 DB 179 GRRITNGTIGRITGLDPAEPCFCQGTPELVRDPSDAKFVDVHTDGAIPVNLGFGMSQV 238  
 QY 237 GHLDYFNGCKHMPGCCDLITPLLKFNFNAYKEMASFFDCNHARSYQFYAESILNPDPAF 296  
 DB 239 GHLDFFNGGVMPGCCCKNLSQI-VDIDIGETGRDFAACNHLRSYKYITDSIVNPDGF 297  
 QY 297 IAYPCRSYTSFKAGNCFECSKGCPTMGHFAFRPHFNKNTN--GSHYFELNTGSLSPFAR 354  
 DB 298 AGPECASVYVFTANKCFPCPSGCGPQMGHYADRY---PGKTDVQKQFYLDGTGASNFAR 354  
 QY 355 WRHKLKSVKLSGEVTOGTVFLRVGGAIGTGEPAIVSGKLEPQNTYKLIADVNAGNIT 414  
 DB 355 WRKVSVYTLSSGKVT-GHILVSLFGNKGNSKQYEIFKGLTKPDSHNSNEFSDVDVGDILQ 413  
 QY 415 SVQFIWKKHLFEDSONKLGAEMVINTSGKYGKYSTPCSDODINGPNILQNLKPC 467  
 DB 414 MVEFIWNNVNTPLRVGASKII-VETNVGQGFNFCSPETVREEVLLTLTPC 465  
 RESULT 11  
 S21223  
 triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - horse (fragment)  
 C:Species: Equus caballus (domestic horse)  
 C>Date: 22-Nov-1993 #sequence\_revision 26-Jul-1996 #text\_change 18-Jun-1999  
 C/Accession: S21223; S21251

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QY      1  MLGIWIVAFLLFFGTSRGCVCYERLGCFKDGLPWTRTFTSTELVGLPWSPEKINRFLLYT  60
DB      1  MLLWLILS-LFLETVAGGVCYFRLGCLGSDNKPWAGTSERPRKGLPWPDPGAINVRFLLYT  59

QY     61  IHNPNAYQEISAVNSSTIQASYGTGDKITRINIAGW--KTDGKWQDMCNVLLQLEIDINC 118
DB     60  NENPNYQIRITA-DSSVIRSSDFKTDKTRFTIHHGFIIDKGEENWLADLCKALFQVESVNC 118

QY    119  INLDWINGSRE-YITHAVNNLRVVGAEVAFIDVLMMKKEFYSKVLHIGLSLGAHLAGEA  177
DB    119  ICDWRGSGRFLYSQASQNIQVGAEVAVLINFLOSQLDYPPSSVHIIHGLSLGAAGEA  178

QY    178  GSRIPG-LGRITGLDPAGPFFHNPKEVRLDPSDANFVDVITHNAARILPELGVGTIDAC  236
DB    179  GRRTNGAIGRITGLDPAEPFYQTPBEIVRLDPSDAQFVDVITHTDGNTPIINPLGFGMSQTV  238

QY    237  GHLDYPYNGGKHMPGCCEDLITPLKKNFNAYKKEMASFFDCNCHARSQFVAESTILNDAF  296
DB    239  GHLDYFFNNGGLQMPGCCOKNLQI--VDIDGIEWGTRDFAACNHLRSKYIIDSITNPKGP  297

QY    297  IAYPCRSYTFKAGNCFCKESKECPWGHFADRFHFKNMKTNGSHGYFLNTGSLSPFAPWR  356
DB    298  AGFSCDSYSSFNKCFPCATGCECPQMGHYADKFPCKT-KENFQNFVLTGDKSNFSRWR  356

QY    357  HKLSVKLSGSEVITQGVFLFVCGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV  416
DB    357  TRIAVTLVSGQKVT-GHVLVSLFDGAGNTKQYEIVRGSUKPNNHNSNEISDSVDVGDGLQKV  415

QY    417  QFIWKHGLFSDSQNKLAGAEVINTSGKYGYKSTFCQSDIMGNFNLQNLKPC  467
DB    416  KFIWNNVNITLPKVGASRIITVTRSD-GRVDFCSQDVTREEVLLTLQPC  465

RESULT 13
JC1318
N:triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - rabbit
N:Alternate names: triglyceride lipase
C:Species: Cryptotagus cuniculus (domestic rabbit)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
C:Accession: JCI318
R:Alaman-Gomez, J.A.; Colwell, N.S.; Sasser, T.; Kumar, V.B.
Biochem. Biophys. Res. Commun. 188, 964-971, 1992
A:Title: Molecular cloning and characterization of rabbit pancreatic triglycerid
F:1-15/Domain: signal sequence #status predicted <SIG>
A:Reference number: JCI318; PMID:93075235; PMID:1445366
A:Accession: JCI318
A:Molecule type: mRNA
A:Residues: 1-465 <ALE>
A:Cross-references: GS:M99365
C:Superfamily: triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase
F:1-15/Domain: signal sequence #status predicted <SIG>
F:170,194,281/Active site: Ser, Asp, His #status predicted

Query Match      43.8%; Score 1107; DB 1; Length 465;
Best Local Similarity 48.1%; Pwd. No. 1.5e-81;
Matches 230; Conservative 74; Mismatches 150; Indels 24; Gaps 13;

QY      1  MLGIWIVAFLLFFGTSRGCVCYERLGCFKDGLPWT-----RTFSTELVGLPWSPEKINTR  55
DB      1  MLLWLALP-LLLGAVALGVCYERLGCFCNRIIPWSGGTLERPFT-----LPSTPKDVNTR  55

QY     56  PLLTYTHNPAYQEIISAVNSSTIQASYGTGDKITRINIAGWKTDGK--WORDMNCVLLQL 113
DB     56  PLLTYNPNPNFQIISA-DASTIRGSNFRTRDKTRFIHGFTDKGENWLSNLCENLQV  114

QY    114  EDINCINLDWINGSR-EYTHAVNNLRVVGAEVAFIDVLMMKKEFYSKVLHIGLSLGAH  172
DB    115  ETVNCICVDWKGSRITYTQAQNTNRIVGAEVAVILVGTLOSSLGYSFNHIVHLSLGAH  174

QY    173  LAGEAGSRIFG-LGRITGLDPAGPFFHNPKEVRLDPSDANFVDVITHNAARILFELGVG  231
DB    175  AAGEVGRRITNGTIGRITGLDPAEPFYQGTPIBRLDPSDAQFVDVITHDAAPVNLGFG  234

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F;170,194,251/Active site: Ser, Asp, His status predicted

Query Match      43.8%; Score 1107; DB 1; Length 465;
Best Local Similarity 48.1%; Pred. No. 1.5e-81;
Matches 230; Conservative 74; Mismatches 150; Indels 24; Gaps 13;

QY      1  MLGIWIVAFIFFGTSRGKVCYERLGCFCQKDLPMT-----RTFSTELVGLPMSPEKINTR 55
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1  MLLWALP-LLLGAVAGLVGVCYERLGCFCGNRPWMSGGTLRPFFST---LFTPKDVNTR 55

QY      56  FLLYTIENPNAYOEIISAVNNSSTIQASYGTDKIRINAGKWTGDK--WORDNCNVLLQL 113
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      56  FLLTYENPNPNFVEISA-DASTIIRSNFTDKRTFIHGFTDKGEWNLNLCENLFPQ 114

QY      114  EDINCINLWDWINGSR-EYTHAVNNLRVVGAEVAFIDVLMMKKFEYSPSKVHLTHGSLGAH 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      115  ETVNCICVDWKGSGSRITYPQATNIRIVGAEVAVLGVLOSSLGYSFNTHVGHSLGAH 174

QY      173  LAGEAGSRIEGLGRITGTDLPDAPGFPHNTPKVERLDPSDANFVDVITHNAARILFELGVG 231
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      175  AAGEVGRRGTNGTIGITGLDPAEPYFOGTPIVRLDPSDAOFVDVITHDAKPPVNLGFG 234
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

232 TIDACGLDFYPNGKHNPGGEDJITLLKFNFNAYKEWAFDCNHFARSQFYAESIL 291  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
235 MSQTGVGHLDFPFGKGKEMFGCQKNVLSQL-VDINGVWEGRTRDFACNHLSRYKYADSIV 293  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
292 NPDAFIAPCRSYTFPKAGNCFFCSKGCPTMGHFADRHFHKMKTN---GSHYPLNTGSL 349  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
294 NPNFAGFCASYTAFSAANKCFPCS-NGCFQMGHYADRF---SRKTDVGQTYFLNTGDS 349  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
350 SPFAWRHKLSVKLGSEVTGGTVFLRVGAIGKTGEFAIVSGKLEPGMTYTKLIDADV 409  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
350 SNFAWRMYQAVTLTSRVRT-GHYLVSLYSGKGNKSQYEFTGLLKPGDTHLNFEPSDVD 408  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
410 VGNITSVFPIWKHLFEDSQNKLAGWVINTSGKYGYKSTFCSDQIMGNILQNLIKPC 467  
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409 VGDVQKVEFWNVNINFTLPKVASQ-IIVEQNDGRVFKFCTDVRREDILLITUPC 465  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

14

glycerol lipase (EC 3.1.1.3) - pig  
ies: Sus scrofa domestica (domestic pig)  
ies: 30-Nov-1980 #sequence revision 22-May-1981 #text\_change 31-Mar-2000  
ssion: A96638; A91256; A90675; J1124; A00732  
aro, J.; Boudouard, M.; Bonicel, J.J.; Guidoni, A.; Desnuelle, P.; Ravery, M.  
.m. Biophys. Acta 671, 129-138, 1981  
.e: Porcine pancreatic lipase. Completion of the primary structure.  
rence number: A90638; MUID:82113655; PMID:7326260  
ssion: A90638  
cule type: protein  
ues: 308-449 <DEC>  
rimental source: pancreas  
ichetta, J.D.; Badaud, J.; Guidoni, A.A.; Bonicel, J.J.; Ravery, M.  
f. Biochem. 97, 395-405, 1979  
.e: Porcine pancreatic lipase. Sequence of the first 234 amino acids of the peptide  
rence number: A91256; MUID:79236335; PMID:380992  
ents: carbohydrate-binding site  
ssion: A91256  
cule type: protein  
ues: 1-234 <BIA>  
rimental source: pancreas  
loni, A.; Bonicel, J.; Bianchetta, J.; Ravery, M.  
mie 61, 841-845, 1979  
.e: Porcine pancreatic lipase. Sequence between the 235th and 307th amino acids.  
rence number: A90675; MUID:80088445; PMID:518929  
ssion: A90675  
cule type: protein  
ues: 235-307 <GUI>  
rimental source: pancreas  
houka, F.; Guidoni, A.A.; De Caro, J.D.; Bonicel, J.J.; Desnuelle, P.A.; Ravery, M.  
f. Biochem. 128, 331-341, 1982  
.e: Porcine pancreatic lipase. The disulfide bridges and the sulfhydryl groups.  
rence number: A91124; MUID:83105095; PMID:7151781  
ents: disulfide bonds  
ssion: A91124  
cule type: protein  
ues: 1-182, 'E', 184-449 <BEN>  
rimental source: pancreas  
loni, A.; Benkouna, F.; De Caro, J.; Ravery, M.  
.m. Biophys. Acta 660, 148-150, 1981  
.e: Characterization of the serine reacting with diethyl p-nitrophenyl phosphate in  
rence number: A90634; MUID:82000578; PMID:6791692  
ents: annotation; substrate-binding site  
ent: Ser-152 reacts with emulsified or micellar diethyl p-nitrophenyl phosphate ar  
rfamily: triacylglycerol lipase  
ords: carboxylic ester hydrolase; glycoprotein; lipid digestion  
1,237-261; 285-296, 299-304, 433-449/disulfide bonds: #status experimental  
01/disulfide bonds: (or 90-103) #status experimental  
Binding site: carbohydrate (Asn) (covalent) #status experimental  
y March 41.1%; Score 1039.5; DB 1; Length 449;  
Local Similarity 48.4%; Pred. No. 4.le-76;

Matches	221; Conservative	62; Mismatches	157; Indels	17; Gaps	12;
Qy	19	EVCYERLGCFCQDGLPWRITFTSELVGLPWSPEK-INTRELLYTIHNPNAYQEISAVNSST	77		
Db	2	EVCFPRLGCFSDADPAGIVORPLKILP--PKQVDVTRFLLYTNQNNYQELVA-DPST	58		
Qy	78	IQASYEGTDKIRIMAGW--KTDGKWORDMCNVLLQLEDINCINLWDINGSRE-YIHAV	134		
Db	59	ITNSNFMORKTRFIHGEIDKEBDMJSLNCKNLFKVESVNCICVDWKGSRTGYTQAS	118		
Qy	135	NNLRVVVGAEVAYFIDVLMKKFYPSPSKVHLHLSIAGHLAGEAGSRIPG-LGRITITGLDPA	193		
Db	119	QNIRIVGAEVAYFVEVLKSSLYGSPSNVHVHIGSLSGSHAAGEAGRRITGTTIERITGLDPA	178		
Qy	194	GPFFHNTPEVELDLPSDANFVDVHITNAARILPELGVGTIDACGHLDFYPNGGKHMPGCE	253		
Db	179	EPFCQGTPELVELDPSDAKFVDVHITDAAPIPNLFGMSQTVGHLDFPFPPNGGQMPGCG	238		
Qy	254	DLITPLLKFNFNAYKKEMASFPDCNHARSYQFYAEASILNPDAFTAYPCRSYTSFKAGNCF	313		
Db	239	KNILSQI-VDIDIGIEWTRDFVACNHLRSYKYADSIILNPDGFAGFFCDSYNVNTANKCF	297		
Qy	314	PCSKECPTMGHFADRFHQMKTNG--SHVFLNTGSLSPFARWRHKLVSXKLSGSSEVTQG	371		
Db	298	PCPSECCPMQGHYADRF---PKGTNGVSQVFLYLTGDAENFARWRYKVSVYTLGSKGVT-G	353		
Qy	372	TVFLRVGGAGTGTGFAIVSGKLEBPGMTYTKLIIDADVNVGNITSVOFIW-KKHLEFDSQN	430		
Db	354	HILVSLFQNGEGRSQVEIYKGTLPDNTSHDSDFSDVEVGLQKVFIWNNVNITLTP	413		
Qy	431	KLGAEMVINTSGKYKSTFCQDIMGNNIILQNLKPC	467		
Db	414	RVGASK-ITVERNDGKVFDFCSQETVREEVLLTNPC	449		

RESULT 15

A28997

N; triacylglycerol lipase (EC 3.1.1.3) precursor, hepatic - human  
N; Alternate names: hepatic triglyceride lipase; lipase; triacylglycerol acylhydrolase, he  
C; Species: Homo sapiens (man)  
C; Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text\_change 18-Jun-1999  
C; Accession: A28997; S00201; A33553; A29932; A35740  
R; Martin, G.A.; Busch, S.J.; Meredith, G.D.; Cardin, A.D.; Blankenship, D.T.; Mao, S.J.T.  
cn, R.L.

J. Biol. Chem. 263, 10907-10914, 1988

A; Title: Isolation and cDNA sequence of human postheparin plasma hepatic triglyceride li  
A; Reference number: A28997; MUID:88273217; PMID:2839510  
A; Accession: A28997  
A; Molecule type: mRNA  
A; Residues: 1-499 <VAR>  
A; Cross-references: GB:J03895; NID:G339594; PIDN:AAA61165.1; PID:G339595  
R; Stahnke, G.; Sprenger, R.; Augustin, J.; Will, H.  
Differentiation 35, 45-52, 1987

A; Title: Human hepatic triglyceride lipase: cDNA cloning, amino acid sequence and expres  
A; Reference number: S00201; MUID:88112595; PMID:2828141  
A; Accession: S00201  
A; Molecule type: mRNA  
A; Residues: 1-255, 'F', 257-499 <STA>  
A; Cross-references: EMBL:X07228; NID:G32497; PIDN:CAA30188.1; PID:G32498  
R; Cai, S.J.; Wong, D.M.; Chen, S.H.; Chan, L.  
Biochemistry 28, 8966-8971, 1989

A; Title: Structure of the human hepatic triglyceride lipase gene.  
A; Reference number: A33553; MUID:90105435; PMID:2605236  
A; Accession: A33553  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 30-255, 'F', 257-499 <CAI>  
A; Cross-references: GB:M92187; GB:J02882; GB:M29189; GB:M29190; GB:M29191; GB:  
A; Note: the authors translated the codon AAT for residue 211 as Ser, CGG for residue 333  
R; Batak, S.; Luo, C.C.; Li, W.H.; VanTuinen, P.; Ledbetter, D.H.; Brown, M.A.; Chen, S.H.  
J. Biol. Chem. 263, 1107-1110, 1988

A; Title: Human hepatic lipase. Cloned cDNA sequence, restriction fragment length polymor

```

:sh completed: January 6, 2004, 11:23:40
:time : 31 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

rotein - protein search, using sw model

1: January 6, 2004, 10:17:33 ; Search time 60 Seconds  
(without alignments)  
2008.509 Million cell updates/sec

US-10-038-517-2

1: score: 2527  
nce: 1 MLGIWIAFLFGTSGKEV.....STFCSQDIMPNTLQNKPC 467

ng table: BLOSUM62

Gapop 10.0 , Gapext 0.5

hed: 830525 seqs, 258052604 residues

number of hits satisfying chosen parameters: 830525

am DB seq length: 0

am DB seq length: 2000000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

ase : SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rhodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score	Query Match	Length	DB ID	Description
1180	46.7	473	11 070478	O70478 mus musculu
1162	46.0	467	4 08TAU2	Q8tau2 homo sapien
1121	44.4	434	11 P81139	P81139 cavia porce
1108	43.8	470	13 Q8QGM1	Q8qgm1 anguilla ja
1106	43.8	465	11 Q9QWF3	Q9qwf3 spermophilu
1098	43.5	465	11 Q88354	Q88354 equus caball
1084	42.9	452	6 Q95KP4	Q95kp4 equus caball
1063	42.1	427	6 Q28287	Q28287 canis fami
1062	42.0	451	11 Q9QUN4	Q9qun4 rattus norv
553.5	22.0	952	5 Q9VX01	Q9vxo1 drosophila
513	20.3	451	4 Q8WY8	Q8wyy8 homo sapien
503	19.9	510	11 Q8VC44	Q8vc44 mus musculu
501.5	19.8	499	6 Q46559	Q46559 oryctolagus
500	19.8	540	5 Q9W448	Q9w448 drosophila
478.5	18.9	452	6 Q9BDJ4	Q9bdj4 oryctolagus
476.5	18.9	510	13 Q98UI2	Q98ui2 pagrus majo

17	476.5	18.9	511	13	Q98UI3
18	475.5	18.8	451	11	Q8CIV3
19	473.5	18.7	449	11	Q8BX85
20	460.5	18.2	490	13	Q9ESV4
21	452	17.9	475	4	Q96FC4
22	449	17.8	449	6	Q95KN9
23	445	17.6	503	13	Q9W6Y2
24	442.5	17.5	474	11	Q8C562
25	403.5	16.0	456	11	P97535
26	402.5	15.9	376	4	Q9UPD2
27	402.5	15.9	456	4	Q9591
28	401.5	15.9	323	4	Q8TBC7
29	398.5	15.8	456	11	Q99U51
30	397.5	15.7	456	11	Q8VI78
31	385.5	15.3	421	11	Q8CI45
32	380.5	15.1	332	6	O77644
33	373	14.8	484	5	Q9VJH1
34	369.5	14.6	411	5	Q9VLU1
35	360.5	14.3	163	11	Q9D950
36	359.5	14.2	394	5	Q9V7V4
37	358.5	14.2	390	5	Q9V9P0
38	341	13.5	676	5	Q9VB94
39	339	13.4	575	5	Q9VOC3
40	336.5	13.3	337	5	Q9VB91
41	325.5	12.9	404	5	Q9W304
42	324.5	12.8	341	5	Q9VB89
43	324.5	12.8	404	5	Q8MYX6
44	323	12.8	337	5	Q9VB92
45	318.5	12.6	172	6	Q9TSB3

#### ALIGNMENTS

#### RESULT 1

O70478 PRELIMINARY; PRT; 473 AA.  
ID O70478  
AC O70478;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Pancreatic lipase related protein 1.  
GN PNLIPLP1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_taxid=10090;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=Swiss Webster; TISSUE=Exorbital lacrimal gland;  
RX MEDLINE=99249620; PubMed=10235541;  
RA Remington S.G., Lima P.H., Nelson J.D.;  
ET "Pancreatic lipase-related protein 1 mRNA in female mouse lacrimal gland.";  
RL Invest. Ophthalmol. Vis. Sci. 40:1081-1090(1999).  
[2]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AF061274; AAC15774.1; -  
DR EMBL; AK028105; BAC25750.1; -  
DR HSSP; P06857; IRP1.  
DR MGD; MGI:97723; Pliiprpl.  
DR InterPro; IPR000734; Lipase.  
DR InterPro; IPR001024; Lipoxigenase LH2.  
DR InterPro; IPR000379; Ser esters\_site.  
DR Pfam; PF00151; lipase; 1.  
DR Pfam; PF01477; PLAT; 1.



PRINTS; PRO0821; TAGLIPASE.  
SMART; SM00308; LH2; 1.  
PROSITE; PS00120; LIPASE SER; 1.  
SEQUENCE 473 AA; 52695 MW; PB11C08E6BBC2763 CRC64;  
  
try Match 46.7%; Score 1180; DB 11; Length 473;  
t Local Similarity 49.0%; Pred.No.2e-93;  
ches 231; Conservative 73; Mismatches 159; Indels 8; Gaps 6;  
  
1 MLGIWIAVAFLEFGTSRGKVCYERLGCDFGLPWTFTSTELVGLPWSPEKINTRFLLYT 60  
1 MLILWTIPLFLGAAQKGVYDNLGCFSDAPWAGTAIRPLKLPWPEKINTRFLLYT 60  
  
61 IHNPNAYQISAVNSSTIOASYFGTDKTRINIAGW--KTDGKWQDMCNVLLQLEDINC 118  
61 NENPNFQTLQSDPSTIEASNFQMDRKTFRFIIHGFDKGDSESWVTDCKKLFEEVEVNC 120  
  
119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKFEYSKVLHIGSLGAHLAGEA 177  
121 ICVDWKKSQATYTOQANNRVVVGQAQVMDILLTEYSYPPSKVHLHIGSLGAHVAGEA 180  
  
178 GSRIPLGRITGLDPAGPPFHTNPKEVRLDPSDANFVDVHTNAARILFELGVGTIDACG 237  
181 GSRTPLGRITGLDPVEANPEGTPEEVRLDPSDADFVDVHTDAAPLIPFLGFGTNQMG 240  
  
238 HLDYPNGGKHPGC-EDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESILNDAP 296  
241 HLDFFNGGQMFEGCKKNALSQIV--DIDGWSGTRDFVACNHLSYKYLESILNDPGF 298  
  
297 IAYPCRSYTSFKAGNCFECSKEGCPMTGHFADRFHFKNMKTNGSHYFLNTGSLSPFARWR 356  
299 AAYPCASYRDFESNCKFCPCDQCGPQMGHYADKF-ANNTSVEPQKFFLNTGAXNFARWR 357  
  
357 HKLSVKLSGSEVTOGTVFLRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVNGVNTSV 416  
358 YRSLTFSGEITV-GQVKVSLFSGNSNTRQCDIFRGIKPGGATHSNEEDAKLDVGTIEKV 416  
  
417 QFIWKHLPDSQNKLGAEWINTSGKYKSTFCSDQIMGNILQNLKPC 467  
417 KFLWNNHVNPSFKVGAAKITVQGEERTENFCSEBTREDILLTLTLC 467  
  
T 2  
Q8TAU2 PRELIMINARY; PRT; 467 AA.  
Q8TAU2;  
01-JUN-2002 (T-EMBLrel. 21, Created)  
01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
Pancreatic lipase-related protein 1.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=PANCREAS;  
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; BC025784; AAH25784.1;  
InterPro; IPR000734; Lipase.  
InterPro; IPR001024; Lipoxigenase LH2.  
InterPro; IPR000379; Ser. estrs\_site.  
Pfam; PF00151; lipase; 1.  
Pfam; PF01477; PLAT; 1.  
SMART; SM00308; LH2; 1.  
PROSITE; PS00120; LIPASE SER; 1.  
SEQUENCE 467 AA; 51833 MW; 7680EAE122E258A3 CRC64;  
  
try Match 46.0%; Score 1162; DB 4; Length 467;  
t Local Similarity 48.6%; Pred.No.6.9e-92;  
ches 229; Conservative 75; Mismatches 159; Indels 8; Gaps 6;

QY 1 MLGIWIAVAFLEFGTSRGKVCYERLGCDFGLPWTFTSTELVGLPWSPEKINTRFLLYT 60  
DB 1 MLIFWTITFLGAAKGVYDNLGCFSDTEPGGTAIRPLKLPWPEKIGTRFLLYT 60  
  
QY 61 IHNPNAYQISAVNSSTIOASYFGTDKTRINIAGW--KTDGKWQDMCNVLLQLEDINC 118  
DB 61 NENPNFQTLQSDPSTIEASNFQMDRKTFRFIIHGFDKGDSESWVTDCKKLFEEVEVNC 120  
  
QY 119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKFEYSKVLHIGSLGAHLAGEA 177  
DB 121 ICVDWKKSQATYTOQANNRVVVGQAQVMDILLTEYSYPPSKVHLHIGSLGAHVAGEA 180  
  
QY 178 GSRIPLGRITGLDPAGPPFHTNPKEVRLDPSDANFVDVHTNAARILFELGVGTIDACG 237  
DB 181 GSKTPLGRITGLDPVEASFESTPEEVRLDPSDADFVDVHTDAAPLIPFLGFGTNQMG 240  
  
QY 238 HLDYPNGGKHPGC-EDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESILNDAP 296  
DB 241 HLDFFNGGSEMPGCKKNALSQIV--DIDGWSGTRDFVACNHLSYKYLESILNDPGF 298  
  
QY 297 IAYPCRSYTSFKAGNCFECSKEGCPMTGHFADRFHFKNMKTNGSHYFLNTGSLSPFARWR 356  
DB 299 AAYPCSYKSPESDKCFPCDQCGPQMGHYADKFGARTSEEQ-QKFFLNTGEASNFARWR 357  
  
QY 357 HKLSVKLSGSEVTOGTVFLRVGGAIGKTGEPAIVSGKLEPGMTYTKLIDADVNGVNTSV 416  
DB 358 YGVSTLTSRTAT-GQIKVALFGNKNTHQYSIFRGILKPGSTHSYBFDKLDVGTIDKV 416  
  
QY 417 QFIWKHLPDSQNKLGAEWINTSGKYKSTFCSDQIMGNILQNLKPC 467  
DB 417 KFLWNNHVNPLPKVGATKITVQGEERTENFCSEBTREDILLTLTLC 467  
  
RESULT 3  
P81139 PRELIMINARY; PRT; 434 AA.  
AC P81139;  
DT 01-JAN-1998 (T-EMBLrel. 05, Created)  
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)  
DE 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
DE Pancreatic lipase related protein 2 (EC 3.1.1.3) (GPL) (Fragment).  
OC Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=PANCREAS;  
RX MEDLINE=93257433; PubMed=8490016;  
RA Hjorth A., Carriere F., Cudrey C., Woldike H., Boel E., Lawson D.M.,  
RA Ferrato F., Cambillau C., Dodson G.G., Thim L., Verger R.;  
RT "A structural domain (the lid) found in pancreatic lipases is absent  
RT in the guinea pig (phospholipase)."  
RL Biochemistry 32:4702-4707(1993).  
CC -!- CATALYTIC ACTIVITY: TRIACYLGLYCEROL + H(2)O = DIACYLGLYCEROL + A  
CC FATTY ACID ANION.  
CC -!- TISSUE SPECIFICITY: PANCREAS.  
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
DR HSP; P54318; 1B08.  
DR InterPro; IPR000734; Lipase.  
DR InterPro; IPR001024; Lipoxigenase LH2.  
DR InterPro; IPR000379; Ser. estrs\_site.  
DR Pfam; PF00151; lipase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PRC0821; TAGLIPASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00120; LIPASE SER; 1.  
KW Hydrolyase; Lipid degradation; Pancreas; Glycoprotein.  
FT NON\_TER 1 1  
FT ACT\_SITE 154 154 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 178 178 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 247 247 CHARGE RELAY SYSTEM (BY SIMILARITY).



ry Match 43.8%; Score 1106; DB 11; Length 465;  
t Local Similarity 47.8%; Pred. NO. 4.8e-87;  
ches 226; Conservative 72; Mismatches 161; Indels 14; Gaps 10;

1 MLGIWIVAEFLFCTSGKVCYERLCGCFKDGLPMTRFTSTELVGLPWSPEKINTREFLYYT 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 MLLVWSLA-LLLGA VAGKEVCYDLRGCSDDSPSGGIVERPLXVLIPWSPADVNTREFLYYT 59  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

61 IHNPAYQEISAVNSTIOASVFGTDKXITRINIAGW--KTGDQWQRDMCNVLLQLEDINC 118  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
60 NEMQNDYQQIITA-DSSRIOSSNFKTNRTREPIIHGFIDKGESWLANNCKMFMQVESVNC 118  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

119 INLDWINGGRE-VIIHAVNNLRVVUGAEVAFYFDLVMKFEPYSKVKHLIGHSLGAHAGEA 177  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
119 ICVDWVGGRGTGYTHASQNIRLVGEVAFYVDFFURTOLGYPNSNVHVIHGSHGSHAAGEA 178  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

178 GSRI PG-LGRITGLDPAGFPFHNTPEKVRLPDPSANFVDVIHTNAARILFELGVGTIDAC 236  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
179 GRRTNGAIGRITGLDPAEPCEBGTBELVRLDPSDAQFVDAIHTDGAPIVPNLGFGMSQTIV 238  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

237 GHLDIFYNGSKHPCGCEDLIPTLLKFNENAYKKEMASFFDCNHARSQFYAESLINPDAP 296  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
239 GHLDFFPNGIEPPGCCQNKLSQI-VDIDGIEWETRDFAAACHNLSRYKYTTDSIYNPTGF 297  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

297 IAYPCRSYTSFRAGNCCFFCSKGGCPTMGHFADRFPHKMNKTN--GSHYFLNTGSLSPFAR 354  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
298 AAFSCASYSVFSANKFCPPCGGCPQMGHYADRY---SGKTNGVGOKFYLTGDKSNFSR 354  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

355 WRHKLSVKULSGSEVTQGVTVFLRVGAIKTKGEFAIVSGKLEPMTYTKUIDADVNVGNIT 414  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
355 WRKYKVSYTLSGQKVT-GHILVSLFNAGNSQXYEIYKGLSHPGYTHSNEFSDVDVGDQLQ 413  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

415 SVQFIWKHLFEDSQNKLAGENVINTSGKYKSTPCSODIMGPNILQNLKXP 467  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
414 RVXFIVWNVINPFLPRVGASS-ISVENDRGVFKFCAETREDVLLTINAC 465  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

T 6  
4 PRELIMINARY; PRT; 465 AA.

O88354  
O88354;  
01-NOV-1998 (TEMBLrel. 08, Created)  
01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
01-OCT-2002 (TEMBLrel. 22, Last annotation update)  
Heart pancreatic lipase (Pancreatic triacylglycerol lipase).  
PL-H OR PTL.  
Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Scuriuridae; Sciurinae;  
Spermophilus.  
NCBI\_TaxID=43179;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Heart;  
MEDLINE=98318668; PubMed=9653197;  
Andrews M.T., Squire T.L., Bowen C.M., Rollins M.B.;  
"Low-temperature carbon utilization is regulated by novel gene activity in the heart of a hibernating mammal."; Proc. Natl. Acad. Sci. U.S.A. 95:8392-8397(1998).  
[2]  
SEQUENCE FROM N.A.  
TISSUE=Heart;  
Andrews M.T., Bauer V.W., Squire T.L., Bowen C.M., Rollins M.B.; Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A.  
TISSUE=Heart;  
Andrews M.T., Bauer V.W., Squire T.L., Bowen C.M., Rollins M.B.; Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
[4]  
SEQUENCE FROM N.A.  
TISSUE=White adipose tissue;  
Bauer V.W., Andrews M.T.;

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.					
[5]					
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Pancreas;				
RC	Squire T.L., Bauer V.W., Lowe M.E., Andrews M.T.;				
RA	"Genomic Organization of the Pancreatic triacylglycerol Lipase Gene in				
RT	a Hibernating Mammal.";				
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AF072993; AAC40162.2; -				
DR	EMBL; AF177403; AAD51124.1; -				
DR	EMBL; AF395870; AAK72259.1; -				
DR	HSP; P16233; LLPB.				
DR	InterPro; IPR000734; Lipase.				
DR	InterPro; IPRO01024; Lipoxygenase LH2.				
DR	InterPro; IPRO00379; Ser_estrs_site.				
DR	Pfam; PF00151; lipase; 1.				
DR	Pfam; PF01477; PLAT; 1.				
DR	PRINTS; PR00821; TAGLIPASE.				
DR	SMART; SM00308; LH2; 1.				
DR	PROSITE; PS00120; LIPASE SER; 1.				
DQ	SEQUENCE 465 AA; 51226 MW; A152FB0CDD01169B CRC64;				
Query Match            43.5%; Score 1098; DB 11; Length 465;					
Best Local Similarity    47.6%; Pred. No. 2.4e-86;					
Matches 225; Conservative 72; Mismatches 162; Indels 14; Gaps 10;					
QY	1	MGIWIAFLFFGSRKKEVCYERLCGPKDGIPWRFTSTELVGLPWPSEKINRFLFYLT	60		
DB	:	: : :	:	:	:
DB	1	MLLVMSLA-LLLGVAGAKEVCYDRLCGFSDSPWGIVERPLKVLPWSPADVNTREFLYT	59		
QY	61	IHNPNAYQIEISAVNSITQASVFGTDKIRIMAGW--KTDCGWDMCNVLLOEDINC	118		
DB	:	: : :	:	:	:
DB	60	NENQDNYYQIITA-DSSRIQSNNFKTRKFIIHGFDKGESWLANKMWFVESVNC	118		
QY	119	INLDWINGSRE-YIHAVNNRVVGAEVAIFDVLMKKFEYSPSKVHLIGHSLGAHAGEA	177		
DB	:	: : :	:	:	:
DB	119	ICVDWKGGSGRTGYTQAQNIRIVGAEVAFVDFLTRQLGSPSNVHVHIGSLGSHAGEA	178		
QY	178	GSRIPG-LGRITTGIDDPAGPFHTNKPEVRLEDSDANFVDVIETNAARTILFELGVTIDAC	236		
DB	:	: : :	:	:	:
DB	179	GRTNGAIGRITGLDPAPFCFGTEGPLVELRLDFSDAQVDIAITGDGAPIVNLGFQMGSQT	238		
QY	237	GHLDYPNGGKHMPGCCBDLITPLLKNFNAYKEMASFPCNHARSYOFYAESILNPDAF	296		
DB	:	: : :	:	:	:
DB	239	GHLDFFPNGGIEMPCCQKNIQSQI-VDIGIWEGTRDPAACNHLRSKYKTTDSIVNPTGF	297		
QY	297	IAYCRSVTSFKAGNCFCKSCGPCPTMGHPADRHFHKWNKTN--CSHYFIANTGSLSFAR	354		
DB	:	: : :	:	:	:
DB	298	AAFSCASYVSFAKNCPCPGSGCPQGHYADRY---SGKTNGVGQKPYLNTGDKSNFSR	354		
QY	355	WHKLKSVLKSGSEYVTOGTVEFLRVGGAGIKGTGFAIVSGLEPGMYTKLIADYNVGNIT	414		
DB	:	: : :	:	:	:
DB	355	WAYKSVTLTSQKYT-GHILVSLFAGNASKQYEIVKLSLHSGYTHSENFSDVDVGDQLQ	413		
QY	415	SVQFTWKXLFDESONKLGAEWINTSGKYGYKTFCSODINGPINLQNLKPCL	467		
DB	:	: : :	:	:	:
DB	414	VYKFTVMNVNINPLSPRGVASS-ISVERNDGRVFRKFCSAETREDVILLTNAC	465		
RESULT 7					
Q9SKP4	ID	Q9SKP4	PRELIMINARY;	PRT;	452 AA.
AC	Q9SKP4;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-WAR-2003 (TREMBLrel. 23, Last annotation update)				
GE	Pancreatic lipase-related protein type 2 (Fragment).				
DE	LIP2.				
OS	Equis caballus (Horse). <sup>t</sup>				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				
OX	NCBI_Taxid=9796;				
RN	[1]				

SEQUENCE FROM N.A.  
 "Jayne S., Kerfelec B., Fogliuzzo E., Chapus C., Crenon I.;  
 "Hoare pancreatic lipase related protein 2 : expression in adult and  
 properties.";  
 Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF359386; AAK38605.1;  
 InterPro; IPR000734; Lipase.  
 InterPro; IPR001024; Lipoxigenase LH2.  
 InterPro; IPR003379; Ser\_estrs\_site.  
 Pfam; PF00151; lipase; 1.  
 Pfam; PF01477; PLAT; 1.  
 PRINTS; PR00821; TAGLIPASE.  
 SMART; SM00308; LH2; 1.  
 PROSITE; PS00120; LIPASE\_SER; 1.  
 NCBI TaxID=9615;  
 SEQUENCE 452 AA; 5063 MW; 386AFA5732D69AD9 CRC64;  
 Query Match 42.9%; Score 1084; DB 6; Length 452;  
 Best Local Similarity 44.6%; Pred. No. 3.7e-85;  
 Matches 209; Conservative 80; Mismatches 144; Indels 36; Gaps 8;  
 18 KEVCYERIGCGKDGLPWTRTSTSTELVGLPWSPEKINTRELLYTHNPAYQEISAVNSST 77  
 1 KEVCYTPGCGSDDKPMAGTLQRLKSLPWSPEEVTRELLYTNKNDPSYQLITARDVAT 60  
 78 IQASVFGTDKTRINIAAGKTDGK--WORDMCNVLLOEDINCINLNDWINGSR-EYIHAV 134  
 51 IKSNFQSRKTHFVHGFDRGDSWPSDMCKILQVETTCISVDWSSGAKAEYQAV 120  
 135 NNLRVGAEVAFYIDVLMKKFEYSPKVLHGLHSLGAHLAGEAGSRIPG-LGRITGLDPA 193  
 121 QNIRIVGAETAYLQILLTELSPENPVNHHGLSGLAHTAGEAGRLRGVRGVTGLDPA 180  
 194 GPFFHNTPEKVRLEPDSANFVDVHTHNAARILFELGVTGDAGCHLDFFPNGKHPGCE 253  
 181 EPCFOADSEVRLEPDSQAQFVDVHTDASPMPLSGFGMSQKQGHMDFFPENGKMPGCK 240  
 254 DLITPLKFNFNAYKEMASFFD-----CNHARSQFYAESILNPDARFAYP 300  
 241 -----RSSFTPIDINGIWQGAQDVLACNHLKSEYYSILNPDGFLAYP 286  
 301 CRSYTSFYAGNCPCFCKEGCTMGHFDADRPHFKMKTNGSHYFLNTGSLSPFARMHKL 360  
 287 CDSYDKFOENGCFPCPAGGCPMGHQAQYKETSQVEQT-FFLNTGESGDYTSWRYVS 345  
 361 VKLSGSEVTQGTVFLRVGAGLGTGEFAIVSGKLEPGMTYTKLIDADVN--VGNITSVQF 418  
 346 ITLASGKANGYLKVTIRGNSGNSKQEIYFGSLQPDSSYI--LDVNVFIKIQIEVKF 403  
 419 IWKXHLFEDSQNKLGAEMVINTSGYKYSTFCSDIMGNPILQNLKPC 467  
 404 VNNKTVLNLKPOLGASRITVQSGADGTEYKFGSGTVDQNVQSLVPC 452  
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 228287 PRELIMINARY; PRT; 427 AA.  
 228287;  
 01-NOV-1996 (TRENBLrel. 01, Created)  
 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 pancreatic lipase.  
 canis familiaris (Dog).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI TaxID=9615;  
 1)  
 SEQUENCE FROM N.A.  
 MEDLINE=89327249; PubMed=250543;  
 Mickel F.S., Weidenbach F., Swarovsky B., LaForge K.S., Scheele G.A.;  
 Structure of the canine pancreatic lipase gene.";  
 . Biol. Chem. 264:12895-12901(1989).  
 EMBL; M28151; AAA30840.1; "

DR EMBL; M28141; AAA30840.1; JOINED.  
 DR EMBL; M28142; AAA30840.1; JOINED.  
 DR EMBL; M28143; AAA30840.1; JOINED.  
 DR EMBL; M28144; AAA30840.1; JOINED.  
 DR EMBL; M28145; AAA30840.1; JOINED.  
 DR EMBL; M28146; AAA30840.1; JOINED.  
 DR EMBL; M28147; AAA30840.1; JOINED.  
 DR EMBL; M28148; AAA30840.1; JOINED.  
 DR EMBL; M28149; AAA30840.1; JOINED.  
 DR EMBL; M28150; AAA30840.1; JOINED.  
 DR HSP; P06857; IRP1.  
 DR InterPro; IPR000734; Lipase.  
 DR InterPro; IPR001024; Lipoxigenase LH2.  
 DR InterPro; IPR003379; Ser\_estrs\_site.  
 DR Pfam; PF00151; lipase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00821; TAGLIPASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00120; LIPASE\_SER; 1.  
 SQ SEQUENCE 427 AA; 47145 MW; 93F3CD4131C15CED CRC64;  
 Query Match 42.1%; Score 1063; DB 6; Length 427;  
 Best Local Similarity 44.9%; Pred. No. 2.2e-83;  
 Matches 211; Conservative 68; Mismatches 145; Indels 46; Gaps 5;  
 QY 1 MLGTWVAFLEFFGTSRCKEYCYERLGCYKDGLPWTRTSTSTELVGLPWSPEKINTRELLY 60  
 DB 1 MVSITWIALFLLGAAKAEVCYEQICGCFSDAEFWAGTAIRPLKVLWPSPERGTRFLLYT 60  
 QY 61 IHNPAYQEISAVNSSTIQASYFGTQDKITRINIAAGW--KTDGKQWQDMCNVLLOEDINC 118  
 DB 61 NKNPNFQTLPSDPSSTIEASNFQDKTETFIHGFIDKGEENWLLDMCKNFKVEVNC 120  
 QY 119 INLDWINGSR-EYIHVNNLRVVGAEVAFYIDVLMKKFEYSPKVLHGLHSLGAHLAGEA 177  
 DB 121 ICVDKKGSGTSYTOAANNRVVVGAGVQAQVMSLSANYSYSPSQVLHGLHSLGAHVAGA 180  
 QY 178 GSRTPGLGRITGLDPAAGPFPHTPKVRLDPSANFVDVHTHNAARILFELGVTGDACG 237  
 DB 181 GSRTPGLGRITGLDPAEASFGQTPPEVRDPTDADFDVHIDAAFLIFLGT----- 233  
 QY 238 HLDYFYPNGKHPGCEDLITPLKFNFNAYKEMASFFDCNARSQFYAESILNPDARF 297  
 DB 234 -----RDFVACNELRSYKYSESILNPDGFA 259  
 QY 298 AYPERSYTSFKAGNCPCFCKEGCTMGHFDADRPHFKMKTNGSHYFLNTGSLSPARWH 357  
 DB 260 SYPCASYRAPESNKKPCPCDQCPQMGHYADKFAVKT-SDETQKFLNTGDSNFAWR 318  
 QY 358 KLSVKLSGSEVTQGTVFLRVGAGLGTGEFAIVSGKLEPGMTYTKLIDADVNNGNITSVQ 417  
 DB 319 GVSTILSGKEAT-GQAKVALFGSKGNTHQFNIFKGLKFGSTHSNEFDKLDVGTIEKV 377  
 QY 418 FIWKXHLFEDSQNKLGAEMVINTSGYKYSTFCSDIMGNPILQNLKPC 467  
 DB 378 FLWNNNVNPTFPKVGAAKITVQGBEKTVHFCSESTVREDVLLTLTPC 427  
 RESULT 9  
 Q9QUN4  
 ID Q9QUN4 PRELIMINARY; PRT; 451 AA.  
 AC Q9QUN4  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Pancreatic lipase (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WISTER-KING; TISSUE=Pancreas;

DT	01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE	CG6847 protein.
DN	CG6847.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RP	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RC	VEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	Georgie R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeoon K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cavay S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.H., Wang X.,
RA	Swirkas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RL	The genome sequence of Drosophila melanogaster.;
DR	Science 287:2185-2195(2000).
DR	EMBL; AE003507; AAF48784.1; ..
DR	HSSP; P29183; IHPL.
DR	FlyBase; FBGN0030884; CG6847.
DR	InterPro; IPR000734; Lipase.
DR	InterPro; IPR000379; Ser esters_site.
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DR	PRINTS; PR00821; FAGLIPASE.
SQ	SEQUENCE 952 AA; 104665 MW; EAC08569B95455CD CRC64;
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Best local similarity 31.4%; Pred. No. 5.8e-39;	
Matches 148; Conservative 72; Mismatches 156; Indels 95; Gaps 14;	
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DB	22 KRCVYELGCFEDSGFF-----AYLEMLPSSPEINTKFYFSTRTORSRPLMELSFUNW 76
QY	64 PNAVQ-----EISAVNSSTIQ-----SY 82
DB	77 TNAFRGKRETEVSTSSPECTSGRSVASAPSSAVNATFTTTERPGGQKKPTSIDDL 136
QY	83 FGDTKLT-RINTAGWKT--DGKQWQEDCNVLQLEDINCINLWDINGSR--EYIFAVNNL 137

[illegible]

137	EGFELSVRVIVHGFSGACPHWYIEMKALTALNAVEDCIVICVDWENGATFPNYVRAAANT	196
138	RVVGAEVAVFIDVLMKKFYSPSKVHLIGHSLAGHAGEAGSRIPLGLGRITGLDPAGPFF	197
197	RLVGKQLAMLLNLQHGKGLDLMTHTVIGSLGAHVSFGAELPGLSRITGLDPLGFLF	256
198	HNTPKVRLDPSDANFVDVHTWAARILFELGVGTIDACGHLDFPVGKEMPGCEDL	255
257	EAQPKVRLDSSDAEFVDVHSGENLILG-GLGSGWQPMGHVDPYTPNGRQVOTGCSNLFV	315
256	--ITPLKFNFNAYKEMASFFDCNHNARSYQFVABSIILNPDAFIAPCRSYTSFKAGNCF	313
316	GAVTDFIWSQAADDEGRSL--CNHRRAYKFIDSVAPRCLFPAFCGNVDDFLKGRCP	373
314	FCSK-----EG---CPTWGHADRFHFKMMKTNHSHYFLNTGSLSPFARWRHKLVS	364
374	PCQDDEDAEGVRCNNGVYADR-----STGRGQYLLTREBEPFCAHQFQIQFNS	427
365	GSEVTQGTFLRVGGAGTGTGFVAVSGKLEPGMTYTKLIDADVNGNITS	415
428	FNDLPURT-----IGRLAILEGGGLNETFEISEKDDAEFPAGDIVS	470
18WY8	PRELIMINARY; PRT; 451 AA.	
18WY8	1-MAR-2002 (TrEMBLrel. 20, Created)	
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
membrane-bound phosphatidic acid-selective phospholipase A1 (Lipase		
1).		
homo sapiens (Human).		
ukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
CB1_TaxID=9608;		
1		
SEQUENCE FROM N.A.		
onoda H., Aoki J., Hiramatsu T., Ishida M., Bando K., Nagai Y.,		
'sujimoto M., Taguchi R., Arai H., Inoue K.,		
A novel phosphatidic acid-selective phospholipase A1 that produces		
ysophosphatidic acid,"		
submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
2		
SEQUENCE FROM N.A.		
EDLINE=2220143; PubMed=12213196;		
in W., Broedl U.C., Monajemi H., Glick J.M., Rader D.J.;		
Lipase H, a New Member of the Triglyceride Lipase Family Synthesized		
y the Intestine,"		
enomics 80:268-273 (2002).		
MEL; AY03612; AAK63178.1; --		
MEL; AY093498; AAM18803.1; --		
new; HGNC:18483; LipH.		
nterPro; IPR000734; Lipase.		
nterPro; IPR000379; Ser.estr. _site.		
fam; PF00151; lipase; 1.		
PRINTS; PR00821; TAGLIPASE.		
SEQUENCE 451 AA; 50859 MW; 949CE32B0C15868B CRC64;		
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1 MLGIMI-VAFLEPFGTSRKEVC--VERLGCCKDGLPWTPTSTELVGLPSPKINTRFL		57
1 MURFYLISLLCLSRDAEETCPSTRL-----SFLSAVVG-----TGLNVRML		44
58 LYTIHNPAYQBEISAVNSSTIQASYFGTDKITRINIAAGWKTDGK---INIAAGWKTDGK---WORDMCNVL		111
45 LYTRKNLTAQ-----TINSAFAGNLNVTKTTFIVHGFRTGSPFPWMDLVKGLL		96
112 QLEDINCINLDWINGSRE--YTHAVNNRVVGAEVAVFIDVLMKKFYSPSKVHLIGHSL		169
137	EGFELSVRVIVHGFSGACPHWYIEMKALTALNAVEDCIVICVDWENGATFPNYVRAAANT	196
138	RVVGAEVAVFIDVLMKKFYSPSKVHLIGHSLAGHAGEAGSRIPLGLGRITGLDPAGPFF	197
197	RLVGKQLAMLLNLQHGKGLDLMTHTVIGSLGAHVSFGAELPGLSRITGLDPLGFLF	256
198	HNTPKVRLDPSDANFVDVHTWAARILFELGVGTIDACGHLDFPVGKEMPGCEDL	255
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256	--ITPLKFNFNAYKEMASFFDCNHNARSYQFVABSIILNPDAFIAPCRSYTSFKAGNCF	313
316	GAVTDFIWSQAADDEGRSL--CNHRRAYKFIDSVAPRCLFPAFCGNVDDFLKGRCP	373
314	FCSK-----EG---CPTWGHADRFHFKMMKTNHSHYFLNTGSLSPFARWRHKLVS	364
374	PCQDDEDAEGVRCNNGVYADR-----STGRGQYLLTREBEPFCAHQFQIQFNS	427
365	GSEVTQGTFLRVGGAGTGTGFVAVSGKLEPGMTYTKLIDADVNGNITS	415
428	FNDLPURT-----IGRLAILEGGGLNETFEISEKDDAEFPAGDIVS	470
18WY8	PRELIMINARY; PRT; 451 AA.	
18WY8	1-MAR-2002 (TrEMBLrel. 20, Created)	
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
membrane-bound phosphatidic acid-selective phospholipase A1 (Lipase		
1).		
homo sapiens (Human).		
ukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
CB1_TaxID=9608;		
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SEQUENCE FROM N.A.		
onoda H., Aoki J., Hiramatsu T., Ishida M., Bando K., Nagai Y.,		
'sujimoto M., Taguchi R., Arai H., Inoue K.,		
A novel phosphatidic acid-selective phospholipase A1 that produces		
ysophosphatidic acid,"		
submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
2		
SEQUENCE FROM N.A.		
EDLINE=2220143; PubMed=12213196;		
in W., Broedl U.C., Monajemi H., Glick J.M., Rader D.J.;		
Lipase H, a New Member of the Triglyceride Lipase Family Synthesized		
y the Intestine,"		
enomics 80:268-273 (2002).		
MEL; AY03612; AAK63178.1; --		
MEL; AY093498; AAM18803.1; --		
new; HGNC:18483; LipH.		
nterPro; IPR000734; Lipase.		
nterPro; IPR000379; Ser.estr. _site.		
fam; PF00151; lipase; 1.		
PRINTS; PR00821; TAGLIPASE.		
SEQUENCE 451 AA; 50859 MW; 949CE32B0C15868B CRC64;		
y Match		
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hes 132; Conservative 62; Mismatches 152; Indels 60; Gaps 15;		
1 MLGIMI-VAFLEPFGTSRKEVC--VERLGCCKDGLPWTPTSTELVGLPSPKINTRFL		57
1 MURFYLISLLCLSRDAEETCPSTRL-----SFLSAVVG-----TGLNVRML		44

291 LNPD-AFIAPCRSYTSFKAGNCFPSKGCPTMGHFAFRPHFKNMKNGSHYFLNTGSL 349  
 292 QHSLSQSIGFQCSDMGFSQCLCLSKCKGRCNTLGYDIR---KDRSGKSKLFLITRAQ 347  
 350 SPFAWRHKLKSVKLSG--SEVTQGVFLRVGGAIGTGFALVSGK-LFPGMTYTKLIDA 406  
 348 SPFKVYHQKFIQFINGIEKRPVPTTMSLGLTKKEIKRIPITLGEIGTSNKYSFLITL 407  
 407 DVVNGNTSVQFIWK--HLFEDSQNKL--GAE-----MVINT---SGKYKSTF 450  
 408 KDIGELLILKFKWNSAVWVNTVQITLWGLIEPHHSLGLILKTIWVKGAGETQRTF 467  
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 468 CPENL 472

PRELIMINARY; PRT; 499 AA.

046559  
 046559;  
 01-JUN-1998 (TrEMBLrel. 06, Created)  
 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 Hepatic lipase.  
 Oryctolagus cuniculus (Rabbit).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 NCBI\_TaxID=9986;  
 [1]  
 SEQUENCE OF 3-499 FROM N.A.  
 MEDLINE=92121762; PubMed=1770315;  
 Warren R.J., Ebert D.L., Mitchell A., Barter P.J.;  
 "Rabbit hepatic lipase cDNA sequence: low activity is associated with  
 low messenger RNA levels";  
 J. Lipid Res. 32:1333-1339(1991).  
 [2]  
 SEQUENCE OF 1-2 FROM N.A.  
 Mitchell A.;  
 "First six bases of rabbit hepatic lipase coding sequence";  
 Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 [3]  
 SEQUENCE FROM N.A.  
 Warren R.J., Ebert D.L., Mitchell A., Barter P.J.;  
 Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF041202; AAB96786.1; --  
 HSP; P06857; 1RP1.  
 InterPro; IPR00734; Lipase.  
 InterPro; IPR001024; Lipoxigenase\_LH2.  
 InterPro; IPR000379; Ser\_estra\_site.  
 Pfam; PF00151; lipase; 1.  
 Pfam; PF01477; PLAT; 1.  
 PRINTS; PR00821; TAGLIPASE.  
 SMART; SM00308; LH2; 1.  
 PROSITE; PS00120; LIPASE\_SER; 1.  
 SEQUENCE 499 AA; 58613 MW; 4DA7D65EE815A0AS CRC64;

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 54 TRFLYFHNPAYQISAVNSTIQASVFGTDKTRINIAWKTDGK-----WORDMCN 108  
 49 TRFLYFK-DRANKGQRLHADTLQECFNSPLVMTVHGVMSVDGLLESIWQMAAL 107  
 109 VLQLEDINCILDWIN-GSEYIHAVNLRVVGAEVYFIDVLMKKYEYSPSKVHLIGH 167  
 108 KQSPARPVNVLGVDWLSLAHSHYAVAVNARLVQGEVAALLQWLESAPPFSNVHLIGY 167  
 168 SLGHLAGAGSRIPG---LGRITGLDPAGPFPHNTPKVRLDPSDANFVDVHNNAARI 224  
 168 SLGHVAGFAGSYISGKHKIGRITGDAAGPLFEGTSASDRILSPDDATFVDAIHT--FTRE 226

225 LPELGYTTIDACHLDPYNGGKHPGCE--DLITPLKFNFNAYKKEMASFFPCNHARS 282  
 227 HNLGSLVGIQPVGHYDFYNGGSGFQPGCHFLYKHAHQGLNA-----LSQTIKAHARS 282  
 283 YQFYABSLNPD-AFIAPCRSYTSFKAGNCFPSKGCPTMGHFAFRPHFKNMK-TNGS 340  
 283 VHLFIDSLHPSMQSTAYQCSMDMSFSQCLGCTKGRCNTLG-----YHIRQPLSKXGK 337  
 341 HVLNLTGSLSPFARWRHKLKSVKLSG--SEVTQGVFLRVGGAIGTGFALVSGK-LFPG 397  
 338 RFLVYTOAGSPRVHYQFKIQFINQIEKPLEPFTMSLGLTKKEMQKIPITLGEIGTSN 397  
 398 MYTKLIDADVNVGNITSVQFIWK--HLFEDSQNKL-----GAEMVINT---S 441  
 398 KTVSELTILNLDIGELMWIKFKWNSAVWVNTVQITLWGLIEPHHSLGLILKTIWVKA 457  
 442 GKYGKSTFCSDI---MGNILQNLKPC 467  
 458 GETQQRMTFCSENMDDQLHPTQEKVFRVC 487

PRELIMINARY; PRT; 540 AA.

03W448  
 03W448;  
 01-MAY-2000 (TrEMBLrel. 13, Created)  
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE CG5966 protein (LD47264P).  
 CG5966.  
 OCS Drosophila melanogaster (Fruit fly).  
 OCS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OCS Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OCS Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=BERKELEY;  
 MEDLINE=20196006; PubMed=10731132;  
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
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 Abril J.F., Achayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
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 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
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 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
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 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,





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tein - protein search, using sw model

n: January 6, 2004, 11:10:48 ; Search time 18 Seconds  
(without alignments)  
1220.082 Million cell updates/sec

st score: 2527  
nce: 1 MGIIWVAFLEFGTSGKEV.....STFCSQDINGPILQNLKPC 467

g table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ted: 127863 seqs, 47026705 residues

number of hits satisfying chosen parameters: 127863

am DB seq length: 0  
am DB seq length: 2000000000

processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

ise : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Query Match	Length	ID	Description
1	1191	47.1	470	1 LIP2 MYOCO	Q64424 myocastor c
2	1172	46.4	473	1 LIP1 RAT	P54316 rattus norv
3	1166	46.1	467	1 LIP1 CANFA	P06857 canis fami
4	1162	46.0	467	1 LIP1 HUMAN	P54315 homo sapien
5	1152	45.6	469	1 LIP2 HUMAN	P54317 homo sapien
6	1147.5	45.4	457	1 LIP2 MYOCO	Q64425 myocastor c
7	1142.5	45.2	468	1 LIP2 RAT	P54318 rattus norv
8	1115	44.1	465	1 LIP2 HUMAN	P16233 homo sapien
9	1109	43.9	461	1 LIP2 HORSE	P29183 equus cabal
10	1108	43.8	465	1 LIP2 CAVPO	P50903 cavia porce
11	1105	43.7	465	1 LIP2 RABIT	Q02157 oryctolagus
12	1094.5	43.3	468	1 LIP2 MOUSE	P17892 mus musculu
13	1073	42.5	465	1 LIP2 RAT	P27657 rattus norv
14	1069	42.3	450	1 LIP2 PIG	P00391 sus scrofa
15	534	21.1	499	1 LIP2 HUMAN	P11150 homo sapien
16	524	20.7	500	1 LIP2 MOUSE	Q9WY95 mus musculu
17	515.5	20.4	500	1 LIP2 HUMAN	Q9YX59 homo sapien
18	499	19.7	510	1 LIP2 HUMAN	P27656 mus musculu
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20	471	18.6	465	1 LIP2 CAVPO	P11153 cavia porce
21	465.5	18.4	475	1 LIP2 MUSVI	Q46647 musccla vis
22	464	18.4	478	1 LIP2 FELCA	P55031 felis silve
23	459	18.2	478	1 LIP2 PIG	P49923 sus scrofa
24	458.5	18.1	490	1 LIP2 CHICK	P11602 gallus gall
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27	450	17.8	475	1 LIP2 PAPAN	P49060 papio anubi
28	445.5	17.6	474	1 LIP2 RAT	Q06000 rattus norv
29	444.5	17.6	465	1 LIP2 BOVIN	P11151 bos taurus
30	441.5	17.5	474	1 LIP2 MOUSE	P11152 mus musculu
31	291	11.5	301	1 PAL POLAN	Q9U6W0 polistes an
32	287	11.4	303	1 PAL2 DOLMA	P53357 dolichovesp
33	284.5	11.3	300	1 PAL1 VESMC	P51528 vespula mac

P49369 vespula vul  
Q06478 dolichovesp  
P02843 drosophila  
P06607 drosophila  
P02844 drosophila  
P27587 ceratitis c  
P27878 ceratitis c  
Q8Vbx1 rattus norv  
P00688 mus musculu  
Q9ce01 lactococcus  
Q28295 canis fami  
P39533 saccharomyc

ALIGNMENTS

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ID LIP2\_MYOCO STANDARD; PRT; 470 AA.  
AC Q64424;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Pancreatic lipase related protein 2 precursor (EC 3.1.1.3) (PL-PP2).  
OS Myocastor coypus (Coypu) (Nutria).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;  
OC Myocastor.  
NCBI\_TaxID=10157;  
RX MEDLINE=95154288; PubMed=7851384;  
RA Thirstrup K., Carriere F., Hjorth S.A., Rasmussen P.B., Nielsen P.F.,  
Ladefoged C., Thim L., Boel E.;  
RT "Cloning and expression in insect cells of two pancreatic lipases and  
a procolipase from Myocastor coypus.";  
RL Eur. J. Biochem. 227:186-193 (1995).  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-23.  
RC TISSUE=Pancreas;  
RX MEDLINE=94176463; PubMed=8130186;  
RA Thirstrup K., Verger R., Carriere F.;  
RT "Evidence for a pancreatic lipase subfamily with new kinetic  
properties.";  
RL Biochemistry 33:2748-2756 (1994).  
CC -!- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a  
fatty acid anion.  
CC -!- TISSUE SPECIFICITY: Pancreas.  
CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
CC -!- SIMILARITY: Contains 1 PLAT domain.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X83000; CAA58121.1; -.  
DR PIR; A54232; A54232.  
DR HSSP; P54318; 1BU8.  
DR InterPro; IPR000734; Lipase.  
DR InterPro; IPR001024; Lipoxigenase LH2.  
DR InterPro; IPR000379; Ser\_estra\_site.  
DR Pfam; PF00151; lipase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00821; TAGLIPASE.  
DR SMART; SMC0308; LH2; 1.  
DR PROSITE; PS00120; LIPASE\_SER; FALSE\_NEG.  
DR PROSITE; PS50095; PLAT; 1.  
KW Hydrolase; Lipid degradation; Pancreas; Glycoprotein; Signal.

SIGNAL	1	18	
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DOMAIN	358	470	PLAT.
ACT_SITE	172	172	CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	196	196	CHARGE RELAY SYSTEM (BY SIMILARITY).
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DISULFID	22	28	BY SIMILARITY.
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Matches	236	Conservative	63	Mismatches	163
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[illegible]

JT 2  
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 STANDARD; PRT; 473 AA.  
 01-OCT-1996 (Rel. 34, Created)  
 01-OCT-1996 (Rel. 34, last sequence update)  
 15-SEP-2003 (Rel. 42, last annotation update)  
 Pancreatic lipase related protein 1 precursor (EC 3.1.1.3).  
 PNLIPRP1 OR PLRP1.  
 Rattus norvegicus (Rat).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus  
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 SEQUENCE FROM N.A.  
 STRAIN=Wistar; TISSUE=Pancreas;  
 MEDLINE=92111786; PubMed=1730292;  
 Wicker-Planquart C.; Puigserver A.;  
 "Primary structure of rat pancreatic lipase mRNA.";  
 FEBS Lett. 296:61-66(1992).  
 !- CATALYTIC ACTIVITY: Triacylglycerol + H2O = diacylglycerol + a  
 fatty acid anion.

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-|- SUBCELLULAR LOCATION: Secreted (Potential).
-|- SIMILARITY: BELONGS TO THE ASHYROLASE SUPERFAMILY. LIPASE FAMILY.
-|- SIMILARITY: Contains 1 PLAT domain.
-|- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE THE PANCREATIC
      LIPASE.
-----
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or send an email to license@isb-sib.ch)

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EMBL; X61925;	CAA43927.1; -
PIR; S20612;	S20612.
HSP; P06857;	IRP1.
InterPro; IPR000734;	Lipase.
InterPro; IPR001024;	Lipoxygenase_LH2.
InterPro; IPR000379;	Ser_estrg_sife.
Pfam; PF00151;	lipase; 1.
Pfam; PF01477;	PLAT; 1.
PRINTS; SMO0821;	TAGLIPASE.
SMART; SM00308;	LH2; 1.
PROSITE; PS00120;	LIPASE_SER; 1.
PROSITE; PS00095;	FLAR; 1.
Hydrolase; Lipid degradation;	Pancreas; Signal.
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121	ICVDMKKGSQTTYTOAANNRVWGAQVAQMIDILVKVNSYSPSKVHLIHGSLGAHVAGA	180		
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299	AYPCRSYKDFESNKCFFCPDQGCQPMGHVADPAGKS-GDEPKQKFFLNTGEAKNFARW	357		
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01-JAN-1988 (Rel. 06, Created)		
01-NOV-1990 (Rel. 16, Last sequence update)		
15-SEP-2003 (Rel. 42, Last annotation update)		
Pancreatic lipase related protein 1 precursor (EC 3.1.1.3).		
PNLIPRP1 OR PLRPI.		
Canis familiaris (Dog).		
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
NCBI_TaxID=9615;		
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SEQUENCE FROM N.A.		
MEDLINE=89327249; PubMed=2502543;		
Mickel F.S., Weidenbach P., Swarovsky B., Laforge K.S., Scheele G.A.;		
"Structure of the canine pancreatic lipase gene."		
J. Biol. Chem. 264:12895-12901(1989).		
[2]		
SEQUENCE FROM N.A.		
MEDLINE=87175472; PubMed=3562437;		
Kerfelec B., Laforge K.S., Puigserver A., Scheele G.;		
"Primary structures of canine pancreatic lipase and phospholipase A2		
messenger RNAs."		
Pancreas 1:430-437(1986).		
[3]		
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).		
ISSUE=Pancreas;		
MEDLINE=98393022; PubMed=9726421;		
Roussel A., de Caro J., Bezine S., Gastinel L., de Caro A.,		
Carriere F., Loydier S., Verger R., Cambillau C.;		
"Reactivation of the totally inactive pancreatic lipase Rp1 by		
structure-predicted point mutations."		
Proteins 32:523-531(1998).		
-/- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a		
fatty acid anion.		
-/- SUBCELLULAR LOCATION: Secreted.		
-/- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.		
-/- SIMILARITY: Contains 1 PLAT domain.		
-/- CAUTION: WAS ORIGINALLY (REF.1 AND REF.2) THOUGHT TO BE THE		
PANCREATIC LIPASE.		
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modified and this statement is not removed from its commercial		
entities requires a license agreement See http://www.isb-sib.ch/announce/		
or send an email to license@sb-sib.ch)		
EMBL; M35302; AAA30885.1; ..		
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PDB; IRPI; 17-JUN-98.		
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InterPro; IPR01024; Lipoxigenase LH2.		
InterPro; IPR000379; Ser_easts_site.		
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pfam; PF01477; PLAT; 1.		
PRINTS; PR00821; TAGLIPASE.		
SMART; SM00308; LH2; 1.		
PROSITE; PS00		



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 PS4317;  
 01-OCT-1996 (Rel. 34, Created)  
 01-OCT-1996 (Rel. 34, Last sequence update)  
 15-SEP-2003 (Rel. 42, Last annotation update)  
 Pancreatic lipase related protein 2 precursor (EC 3.1.1.3).  
 PNLIP2 OR PLRP2.  
 Homo sapiens (Human).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 SEQUENCE FROM N.A.  
 TISSUE=Pancreas;  
 MEDLINE=92355622; PubMed=1379599;  
 Giller T., Buchwald P., Blum-Kaelin D., Hunziker W.;  
 "Two novel human pancreatic lipase related proteins, hPLRP1 and  
 hPLRP2. Differences in colipase dependence and in lipase activity.";  
 J. Biol. Chem. 267:16509-16516(1992).  
 [2]

SEQUENCE FROM N.A.  
 TISSUE=Pancreas;  
 MEDLINE=22388257; PubMed=12477932;  
 Strausberg R.L., Feitgold E.A., Grouse L.H., Derge J.G.,  
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 Altshul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
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 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
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 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
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 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
 fatty acid anion.  
 -1- TISSUE SPECIFICITY: Pancreas.  
 -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
 -1- SIMILARITY: Contains 1 PLAT domain.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; M93284; AAAS9533.1;  
 EMBL; BC005989; AAH05989.1;  
 PIR; B43357; B43357.  
 HSP; P54318; 1BUB.  
 Genew; HGNC:9157; PNLIPR2.  
 MIM; 604423;  
 GO; GO:0005576; C:extracellular; TAS.  
 GO; GO:0004806; P:triacylglycerol lipase activity; TAS.  
 GO; GO:0006641; P:triacylglycerol metabolism; TAS.  
 InterPro; IPR000734; Lipase.  
 InterPro; IPR001024; Lipoxigenase\_LH2.

InterPro; IPR000379; Ser\_estrs\_site.  
 Pfam; PF00151; lipase; 1.  
 Pfam; PF01477; PLAT; 1.  
 PRINTS; PRO0821; TAGLIPASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00120; LIPASE SER; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 KW Hydrolase; Lipid degradation; Pancreas; Glycoprotein; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 469  
 FT DOMAIN 357 469  
 FT ACT\_SITE 171 171  
 FT ACT\_SITE 195 195  
 FT ACT\_SITE 282 282  
 FT DISULFID 21 27  
 FT DISULFID 109 120  
 FT DISULFID 256 280  
 FT DISULFID 304 315  
 FT DISULFID 318 323  
 FT DISULFID 453 469  
 FT CARBOHYD 353 353  
 FT CARBOHYD 428 428  
 SQ SEQUENCE 469 AA; 51946 MW; DOEL130295A94A725 CRC64;

Query Match 45.6%; Score 1152; DB 1; Length 469;  
 Best Local Similarity 47.8%; Pred. No. 1.1e-87;  
 Matches 225; Conservative 68; Mismatches 172; Indels 6; Gaps 5;  
 QY 1 MGIWIVAFPLPTGSRGKVCVERLQKCPKGLPWTRFSTELVGLPWSPEKINTRFLLYT 60  
 DB 1 MLPPWTGLLLATVGRGEVYQGLGCSDEKPKAGTLQRPVKLLPWSPEIDTRFLLYT 60  
 QY 61 IHPNAYQEISAVNSSTIOASYFGTDKITRINIAGW--KTDGKQWQDMCNVLLQLEDINC 118  
 DB 61 NENPNFOLITGTEPTIEAGNFOLDKRTFIIHGFLDKAEDSWESDMCKMKEVEKVCNC 120  
 QY 119 INLDWINGSRE-YIHANNVNLVGAENVAYFIDVLKKEFYSPSKVHLIGHSLGAHLAGEA 177  
 DB 121 ICVDRHGRSRAMYTOAVQVIRVGAETAFLQALSTQLGVSLESDVHVIGHSLGAHTAAEA 180  
 QY 178 GSRIPG-LGRITGLDPPAGFPFHNTKPEVRLPDPSDANFVDVHTNAARILFELGVGTIDAC 236  
 DB 181 GRRLGRVGRITGLDPPAGFCQDEPVEVRLPDPSDAVFDVHTDSSPIVSLGFGMSQKV 240  
 QY 237 GHLDYPNGGKMPCCEDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESILNPDFA 296  
 DB 241 GHLDYFPNGGKMPCKKNVLSITIT-DIDGIGWEGIGGVSCNHLRSFEYSSVLPNDGF 299  
 QY 297 IAYPCRSYTSFKAGNCPFCSEKQCPQTMGHFADRFHFKNMKNGSHVFLNTGSLSPFARWR 356  
 DB 300 LGYPCASVDETSQSKCPFCPCPAEGCPKMGHYADQFKGKTSAVEQT-FFLNTGESGNFTSWR 358  
 QY 357 HKLSVKLSGSEVTOGTVFLRVGGAIGKTGFEFAIVSGKLBPFGMTYTKLIDADVNGNITSV 416  
 DB 359 YKVSVTLSCKEKWNGYIRIALYGSNENSKQVEIFKGLKPDASHTCAIDVDVFNVGKIQV 418  
 QY 417 QPIWKHLFPESQNKLGAEWINTSGYGVKSTFCSDODINGPILQNLKPC 467  
 DB 419 KFLMNNKGINLSKPLGASQITVQSGEDGTEYNFCSSDTEVENVQLSLYPC 469

RESULT 6  
 LIPP MYOC  
 ID LIPP MYOC STANDARD; PRT; 457 AA.  
 AC Q64425;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Triacylglycerol lipase, pancreatic precursor (EC 3.1.1.3) (Pancreatic  
 lipase) (PL) (Fragment).  
 GN PNLIP.  
 OS Myocastor corpus (Coryu) (Nutria).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Hystricognathi; Myocastoridae;  
Myocastor.

NCBI\_TaxID=10157;

[1] SEQUENCE FROM N.A.

TISSUE=Pancreas;

MEDLINE=9515488; PubMed=7851384;

Thisstrup K., Carriere F., Hjorth S.A., Rasmussen P.B., Nielsen P.F.,

Ladefoged C., Thim L., Boel E.;

"Cloning and expression in insect cells of two pancreatic lipases and

a procolipase from Myocastor coypus.";

Eur. J. Biochem. 227:186-193 (1995).";

-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a

fatty acid anion.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.

-!- SIMILARITY: Contains 1 PLAT domain.

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EMBL: X82959; CAA58120.1; .

PIR: I48206; I48206.

HSSP: P29183; LHPL.

InterPro: IPR000734; Lipase.

InterPro: IPR001024; Lipoxigenase LH2.

InterPro: IPR000379; Ser\_eatrs\_site.

Pfam: PF00151; lipase; 1.

Pfam: PF01477; PLAT; 1.

PRINTS: PRO0821; TAGLIPASE.

SMART: SM00308; LH2; 1.

PROSITE: PS00120; LIPASE SR; 1.

PROSITE: PS00095; PLAT; 1.

Hydrolase; Lipid degradation; Pancreas; Glycoprotein; Signal.

NON TER 1 1

SIGNAL <1 7

CHAIN 347 457 TRIACYLGLYCEROL LIPASE, PANCREATIC.

DOMAIN 347 457 PLAT.

ACT\_SITE 161 161 CHARGE RELAY SYSTEM (BY SIMILARITY).

ACT\_SITE 185 185 CHARGE RELAY SYSTEM (BY SIMILARITY).

ACT\_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).

DISULFID 12 18 BY SIMILARITY.

DISULFID 99 110 BY SIMILARITY.

DISULFID 246 270 BY SIMILARITY.

DISULFID 294 305 BY SIMILARITY.

DISULFID 308 313 BY SIMILARITY.

DISULFID 441 457 BY SIMILARITY.

CARBOHYD 343 343 N-LINKED (GLCNAC...) (POTENTIAL).

SEQUENCE 457 AA; 50209 MW; 33D572B770459DAD CRC64;

ery Match

st Local Similarity 45.4%; Score 1147.5; DB 1; Length 457;

tches 232; Conservative 69; Mismatches 149; Indels 15; Gaps 10;

10 LFFGTSRGKVEYERLGCFLKPLWTRTFSTELVGLPWSPEKINTRELLYTHNPAYQE 69

1 LLLGAVASEVICYDLRGCFSDSPWAGIVERPLKVLWPSPTINTRELLYTHNPAYQI 60

70 ISAVNSSTIQASYFGTKITRINAGW--KTDGKWRDMCNVLLQLEDINCINLDWINGS 127

61 VTA-DSSITRSNFRTRDKTRFIHGYIDKGEENLANMCEALLQVESVNCICVDNMGKS 119

128 RE-YIHVNNLEWCAEYAVFDVLMKKFEYSPKVLHIGSLGAHLAGEAGSRIG-LG 185

120 RALYQTATQINRWGAEYAVFDVLMKKFEYSPKVLHIGSLGAHLAGEAGSRIG-LG 179

186 RITGLDPAEPFPHNTPEKVRDPDANFVDVHNNAAIRILFELGVGTIDACGHLDFYPNG 245

Db 180 RITGLDPAEPFPHNTPEKVRDPDANFVDVHNNAAIRILFELGVGTIDACGHLDFYPNG 239

QY 246 GKHWPGCE-DLITPLKFNFNAYKKNWASFFDCNCHARSYQFYAESILNPDATAYPCRY 304

Db 240 GVEMPGCKNIISQIV--DINGIWEGRTRDFAACNHLRSYKYIDSILNPTGFAGFSCSY 297

QY 305 TSPKAGNCFCCSGECGPTMGHFAFRHFKNMKTNG--SHYFLNTGSLSPFARWRHKLVS 362

Db 298 NTFSSNCCFPCCASGGCPQMGHYADRF--SGKTNELFQQFYLTNGDASNFSRWRYQIATV 354

QY 363 LSGSEVTCQTVFLRVAAGAIKGTGEFAISVGLKLPQGMVTKLIDADVNGNITISVQFIWKK 422

Db 355 LSGHKVT-GHVLVSLYSGSGTSKQYIYKLSGLQFGTSYVNVQIDSDVDVGDIEKVKFIWYN 413

QY 423 HLFEDSQNKLGAEWVINTSGKYKSTFCSDIMGNILQNLKPC 467

Db 414 NIINPTLPKVGCSS-IQVTRDGRVNFCSQDIVREDILLTLTPC 457

# RESULT 7

LIP2\_RAT

ID\_LIP2\_RAT

STANDARD; PRT; 468 AA.

AC P54318;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Pancreatic lipase related protein 2 precursor (EC 3.1.1.3) (Secretory

DE Glycoprotein GP-3)

GN PNLIPR2 OR PLRP2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

SEQUENCE FROM N.A., AND SEQUENCE OF 17-46.

RC STRAIN=Sprague-Dawley; TISSUE=Pancreas;

RX MEDLINE=93252914; PubMed=8486693;

RA Wishart M.J., Andrews P.C., Nichols R., Blevins G.T. Jr.,

RA Logsdon C.D., Williams J.A.;

RT "Identification and cloning of GP-3 from rat pancreatic acinar

RT zymogen granules as a glycosylated membrane-associated lipase.";

RL J. Biol. Chem. 268:10303-10311(1993).

RN [2]

SEQUENCE FROM N.A.

RX MEDLINE=94262798; PubMed=8203536;

RA Payne R.M., Sims H.P., Jennens M.L., Lowe M.E.;

RT "Rat pancreatic lipase and two related proteins: enzymatic properties

RT and mRNA expression during development.";

RL Am. J. Physiol. 266:G914-G921(1994).

RN [3]

X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 17-468.

RC TISSUE=Pancreas;

RX MEDLINE=99041983; PubMed=9822688;

RA Roussel A., Yang Y., Ferrato F., Verger R., Cambillau C., Lowe M.;

RT "Structure and activity of rat pancreatic lipase-related protein 2.";

RL J. Biol. Chem. 273:32121-32128(1998).

CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a

fatty acid anion.

CC -!- SUBCELLULAR LOCATION: SECRETED OR MEMBRANE-ASSOCIATED

CC -!- TISSUE SPECIFICITY: PANCREAS. PANCREATIC SECRETORY (ZPMOGEN)

CC GRANULE.

CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.

CC -!- SIMILARITY: Contains 1 PLAT domain.

CC -----

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

EMBL; L09216; AAA41250.1; ALT\_INIT.

PDB; 1BU8; 23-DEC-98.  
 InterPro; IPR000734; Lipase.  
 InterPro; IPR01024; Lipoxigenase LH2.  
 InterPro; IPR000379; Ser\_estra\_site.  
 Pfam; PF00151; lipase; 1.  
 Pfam; PF01477; PLAT; 1.  
 PRINTS; PR00821; TAGLIPASE.  
 SMART; SMO0308; LH2; 1.  
 PROSITE; PS00120; LIPASE\_SER; 1.  
 PROSITE; PS00095; PLAT; 1.  
 Hydrolase; Lipid degradation; Pancreas; Glycoprotein; Signal;  
 Membrane; 3D-structure.  
 SIGNAL 1 16  
 CHAIN 17 468  
 DOMAIN 356 468  
 ACT\_SITE 170 170  
 ACT\_SITE 194 194  
 CHARGE RELAY SYSTEM.  
 ACT\_SITE 281 281  
 CHARGE RELAY SYSTEM.  
 DISULFID 20 26  
 DISULFID 108 119  
 DISULFID 255 279  
 DISULFID 303 314  
 DISULFID 317 322  
 DISULFID 452 468  
 CARBOHYD 352 352  
 STRAND 18 20  
 HELIX 22 24  
 STRAND 26 28  
 TURN 31 32  
 STRAND 36 36  
 TURN 37 38  
 STRAND 39 39  
 HELIX 48 51  
 TURN 52 52  
 STRAND 54 59  
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 TURN 74 74  
 HELIX 75 78  
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 TURN 84 85  
 STRAND 87 92  
 TURN 98 99  
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 STRAND 301 302  
 HELIX 306 310  
 TURN 311 312

N-LINKED (GLCNAC. . .) (POTENTIAL).

FT TURN 319 320  
 FT STRAND 324 324  
 FT HELIX 327 331  
 FT TURN 333 336  
 FT STRAND 341 345  
 FT TURN 351 352  
 FT STRAND 356 365  
 FT STRAND 370 380  
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 FT TURN 397 398  
 FT STRAND 400 407  
 FT STRAND 414 422  
 FT STRAND 433 442  
 FT TURN 443 445  
 FT STRAND 448 452  
 FT STRAND 457 457  
 FT TURN 459 460  
 FT STRAND 463 468  
 SQ SEQUENCE 468 AA; 52534 MW; B41PB0B339BA9A6F CRC64;

Query Match 45.2%; Score 1142.5; DB 1; Length 468;  
 Best Local Similarity 48.6%; Pred. No. 6.7e-87;  
 Matches 229; Conservative 63; Mismatches 172; Indels 7; Gaps 6;

QY 1 MGIWIVAFPFGRSGKEVYERLGCDFKDLFWTRTFSTELVGLPWSPEKINTRFLLYT 60  
 DB 1 MLLCWIVS-LLLATVGGKEVCYGHLCFSNDKPKWAGMLQRLKIFPWSPEIDITRFLLYT 59  
 QY 61 IHNPNAYQETISAVNSSTIQASYFGTDXITRINAGW--KTDGKQKQDMCNVLLQLEDINC 118  
 DB 60 NENPNYQKISATEPDTIKFSNQLDKRTRFI VHGFIDKGEDGMLDMCKMPQVEKVC 119  
 QY 119 INLDWINGSR-EYIHAVNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177  
 DB 120 ICVDWRGRSREYTCASYNTFVVGAEIAFLVQLVSTEMGYSPENVHLIGHSLGAHVGEA 179  
 QY 178 GSRIPG-LGRITGLDPAGPFHNTPKVRLDPSDANFVDVHTNAARILFELGVGTIDAC 236  
 DB 180 GRLEGHVGRITGLDPAEPFCQGLPBEVRLDPSDANFVDVHTDSAPIIPYLGFGMSQKV 239  
 QY 237 GHLDYPNGGKHPGCCDLITPLLKFNFNAYKEMASFPDCNHARSYQVFAESILNPDAF 296  
 DB 240 GHLDFFPNGKEMPGCCQKNLSTI-VDINGIEGTQNFVACNHLRSYKYIASSILNPDPG 298  
 QY 297 IAYPCRSYTSFKAGNCFFCSKGCPTMGHFAFRHFKNMKMGSHYFLNMGTSLSPPFARWR 356  
 DB 299 LGYPCSSYEFQNDCCPCEGCPKMGHVADQFEGKTATVEQTVY-LNTGDSGNFTWR 357  
 QY 357 HKLSVKLSGSEVTQGTVFLRVGGAIGKTGEFALVSKLEPGMTYTKLIDADVNVGNITSV 416  
 DB 358 YKSVTLUSGAKLSGYILVALYGNNGSKQYEIFKGLSKEARHVRDIDVDINVGSIQKV 417  
 QY 417 QFIWKHLFEDSQNKLGAEWVINTSGKYGVKSTFCSDIMGNILQNLKPC 467  
 DB 418 KFLWNKVINLFRPTILGASQITVQSGVDGKYNFCSSDITVREDVLQSLYPC 468

# RESULT 8

LIPP HUMAN  
 ID LIPP HUMAN STANDARD; PRT; 465 AA.  
 AC P16233;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Triacylglycerol lipase, pancreatic precursor (EC 3.1.1.3) (Pancreatic  
 DE lipase) (PL).  
 GN PNLIIP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

[1] SEQUENCE FROM N.A.  
MEDLINE=90062115; PubMed=2479644;  
Lowe M.E., Rosenblum J.L., Straus A.W.;  
"Cloning and characterization of human pancreatic lipase cDNA.";  
J. Biol. Chem. 264:20042-20048 (1989).

[2] SEQUENCE FROM N.A.  
TISSUE=Pancreas;  
MEDLINE=92355622; PubMed=1379598;  
Giller T., Buchwald P., Blum-Kaelin D., Hunziker W.;  
"Two novel human pancreatic lipase related proteins, hPLRP1 and  
hPLRP2. Differences in colipase dependence and in lipase activity.";  
J. Biol. Chem. 267:16509-16516 (1992).

[3] SEQUENCE FROM N.A.  
MEDLINE=94010322; PubMed=8406023;  
Sims H.F., Jennens M.L., Lowe M.E.;  
"The human pancreatic lipase-encoding gene: structure and  
conservation of an Alu sequence in the lipase gene family.";  
Gene 131:281-285 (1993).

[4] SEQUENCE FROM N.A.  
TISSUE=Lung;  
MEDLINE=22388257; PubMed=12477937;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[5] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
MEDLINE=90158821; PubMed=2106079;  
Winkler F.K., D'Arcy A., Hunziker W.;  
"Structure of human pancreatic lipase.";  
Nature 343:771-774 (1990).

[6] X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
MEDLINE=92396238; PubMed=1522902;  
van Tilbeurgh H., Sarda L., Verger R., Cambillau C.;  
"Structure of the pancreatic lipase-procolipase complex.";  
Nature 359:159-162 (1992).

[7] X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
MEDLINE=93241293; PubMed=8479519;  
van Tilbeurgh H., Egloff M.-P., Martinez C., Rugani N., Verger R.,  
Cambillau C.;  
"Interfacial activation of the lipase-procolipase complex by mixed  
micelles revealed by X-ray crystallography.";  
Nature 362:814-820 (1993).

-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
fatty acid anion.  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
-!- SIMILARITY: Contains 1 PLAT domain.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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CC DR EMBL; J05125; AAA36740.1; -  
CC DR EMBL; M93285; AAA60129.1; -  
CC DR EMBL; L24529; AAA99053.1; -  
CC DR EMBL; L11242; AAA99053.1; JOINED.  
CC DR EMBL; L24502; AAA99053.1; JOINED.  
CC DR EMBL; L24522; AAA99053.1; JOINED.  
CC DR EMBL; L24523; AAA99053.1; JOINED.  
CC DR EMBL; L24525; AAA99053.1; JOINED.  
CC DR EMBL; L24526; AAA99053.1; JOINED.  
CC DR EMBL; L24527; AAA99053.1; JOINED.  
CC DR EMBL; L24528; AAA99053.1; JOINED.  
CC DR EMBL; BC014309; AAHL4309.1; -  
CC DR PIR; C43357; C43357.  
CC DR PDB; 1LPA; 01-NOV-94.  
CC DR PDB; 1LPE; 01-NOV-94.  
CC DR PDB; 1GPL; 12-FEB-97.  
CC DR PDB; 1N8S; 18-DEC-02.  
CC DR Genew; HGNC:9155; PNLP.  
CC DR MM; 246600; -  
CC DR GO; GO:0004806; F:triacylglycerol lipase activity; TAS.  
CC DR InterPro; IPR000734; Lipase.  
CC DR InterPro; IPR001024; Lipoxigenase LH2.  
CC DR InterPro; IPR000379; Ser esters\_site.  
CC DR Pfam; PF00151; lipase; 1.  
CC DR Pfam; PF01477; PLAT; 1.  
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CC DR SMART; SMC0308; LH2; 1.  
CC DR PROSITE; PS00120; LIPASE\_SER; 1.  
CC DR PROSITE; PS50095; PLAT; 1.  
CC KW Hydrolase; Lipid degradation; Pancreas; Glycoprotein; Signal;  
CC KW 3D-structure.  
CC FT SIGNAL 1 16  
CC FT CHAIN 17 465 TRIACYLGLYCEROL LIPASE, PANCREATIC.  
CC FT DOMAIN 355 465 PLAT.  
CC FT ACT\_SITE 169 169 CHARGE RELAY SYSTEM.  
CC FT ACT\_SITE 193 193 CHARGE RELAY SYSTEM.  
CC FT ACT\_SITE 280 280 CHARGE RELAY SYSTEM.  
CC FT DISULFID 20 26  
CC FT DISULFID 107 118  
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CC FT DISULFID 302 313  
CC FT DISULFID 316 321  
CC FT DISULFID 449 465  
CC FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .).  
CC FT STRAND 18 21  
CC FT TURN 22 24  
CC FT STRAND 25 28  
CC FT TURN 31 33  
CC FT HELIX 48 51  
CC FT STRAND 54 58  
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CC FT HELIX 73 78  
CC FT TURN 83 84  
CC FT STRAND 87 91  
CC FT TURN 94 95  
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CC FT HELIX 170 180  
CC FT TURN 181 184  
CC FT STRAND 188 192



STRAND 195 195  
TURN 197 201  
TURN 204 206  
HELIX 210 212  
STRAND 216 219  
TURN 227 229  
STRAND 233 233  
STRAND 241 245  
TURN 246 247  
TURN 252 253  
HELIX 258 262  
TURN 263 263  
TURN 265 266  
HELIX 268 291  
TURN 292 292  
TURN 294 297  
STRAND 298 298  
STRAND 300 301  
HELIX 305 309  
TURN 310 311  
TURN 318 319  
STRAND 323 323  
TURN 326 327  
HELIX 328 330  
TURN 332 335  
STRAND 340 344  
STRAND 355 365  
STRAND 368 378  
TURN 379 380  
STRAND 381 382  
STRAND 386 389  
TURN 395 396  
STRAND 398 405  
STRAND 412 420  
TURN 426 427  
STRAND 431 440  
TURN 441 442  
STRAND 445 449  
STRAND 454 454  
TURN 456 457  
STRAND 460 465  
SEQUENCE 465 AA; 51157 MW; 2B4C9CC7F0E2DF52 CRC64;

RY Match 44.1%; Score 1115; DB 1; Length 465;  
t-Local Similarity 47.8%; Pred. No. 1.3e-84;  
Ches 226; Conservative 73; Mismatches 160; Indels 14; Gaps 10;

1 MLCIIVAPLFGTGRGKVCYERLGCDFKGLPWTRTFSTELVGLPKSPKINTEFLLYT 60  
1 MLPLWTL-LLLGAVAGKEVCYERLGCSDSPSGTTERPLHLPPSPKDVNTRFLLYT 59

61 IHNPNAYQISAVNSSTTQASVFGDKITRINIAGW--KTDGKQWDMCNVLLQLEDINC 118  
60 NENPNFQEVAA--DSSSISGNSFKTNKTRTPIHGFIDKGBEENLANVCNLPKVSVC 118

119 INLDWNGSRE-YIHAVNLRVGAEVAYFDVLMKKFEYSPSKVHLIGHSLGNAHAGEA 177  
119 ICVDNKGSGRTGYTQASQNRIRVGAEVAYFEVFLQSAFGYSPSNVHVHISLGAHAGEA 178

178 GSRIFG-LGRITGLDPAGFPFFHTPKEVRLDPSDANFVDVHTNAARILPELGVGTIDAC 236  
179 GRTNGTIGRTIGLDPAPCPQGTPELVRDPSDAKFVDVHTDGAPIVNLFGMSQVV 238

237 GHLDFYPGKGKMPCEDLITPLKFNENAYKEMASFFDCNHRASQVFAESILNPDAP 296  
239 GHLDFPFGGEMPGCKNHLISQI--VDIDGIEWGTRDFAACNHLRSYKYTDSIVNPDGF 297

297 IAYPCRSYTSFKAGNCFCKSGEGCPTMGHFADRHFKNMKTN--GSHYFLNTGSLSPEAR 354  
298 AGFPACASNVFTANKCFPCGGGCPQNGHYADRY---PGKTNVQKQFYLDTDGASNFAR 354

355 WHHKLKSVKLSGEVTOGTQVFLRVGAIGKTEFAIVSGKLEPQNTYTKLIDADVNGNIT 414

Db 355 WRYKVSVTLGSKKVT-GHILVSLFGNKGNSKQYEIFKGTLPKDPSTHNSFDSVDVGDQL 413  
QY 415 SVQFIWKXHLFEDSQNLGAEMVINTSGKYGVKSTFCQSODIMGNILQNLKPC 467  
Db 414 MKFTWYNNVINPTLPRVGASKII-VEINVGKQNFCSPEIVREEVLLTLTPC 465

RESULT 9  
LIPP\_HORSE  
ID LIPP HORSE STANDARD; PRT; 461 AA.  
AC P29183;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Triacylglycerol lipase, pancreatic precursor (EC 3.1.1.3) (Pancreatic lipase) (PL) (fragment).  
GN PNLIP.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactylia; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=94267022; PubMed=1587279;  
RA Kerfelec B., Foglizzo E., Bonicel J., Bougis P.E., Chapus C.;  
RT "Sequence of horse pancreatic lipase as determined by protein and  
RT cDNA sequencing. Implications for p-nitrophenyl acetate hydrolysis by  
RT pancreatic lipases.";  
RL Eur. J. Biochem. 206:279-287(1992).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RX MEDLINE=94238688; PubMed=8182745;  
RA Bourne Y., Martinez C., Kerfelec B., Lombardo D., Chapus C.,  
RA Cambilliau C.;  
RT "Horse pancreatic lipase. The crystal structure refined at 2.3-A  
RT resolution.";  
RL J. Mol. Biol. 238:709-732(1994).  
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
CC fatty acid anion.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
CC -!- SIMILARITY: Contains 1 PLAT domain.

-----  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; X66218; CAA46961.1; --  
PIR; S21223; S21223.  
PDB; 1HPL; 31-MAY-94.  
InterPro; IPR000734; Lipase.  
InterPro; IPR001024; Lipoxigenase\_LH2.  
InterPro; IPR000379; Ser\_estrs\_site.  
Pfam; PF00151; lipase; 1.  
Pfam; PF01477; PLAT; 1.  
PRINTS; PR00821; TAGLIPASE.  
SMART; SM00308; LH2; 1.  
PROSITE; PS00120; LIPASE\_SER; 1.  
PROSITE; PS50095; PLAT; 1.  
KW Hydrolase; Lipid degradation; Pancreas; Signal; 3D-structure.  
FT NON\_TER <1 1  
FT SIGNAL <1 12  
FT CHAIN 13 461 TRIACYLGLYCEROL LIPASE, PANCREATIC.  
FT DOMAIN 351 461 PLAT.  
FT ACT\_SITE 165 165 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 189 189 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 276 276 CHARGE RELAY SYSTEM.  
FT DISULFID 16 22  
FT DISULFID 103 114

DISULFID 250 274  
DISULFID 298 309  
DISULFID 312 317  
MUTAGEN 445 461  
165  
S->X: 80% LOSS OF P-NITROPHENYL ACETATE  
HYDROLYSIS ACTIVITY.  
STRAND 14 17  
TURN 18 20  
STRAND 21 24  
TURN 27 28  
STRAND 32 32  
TURN 33 34  
STRAND 35 35  
HELIX 44 47  
STRAND 50 55  
TURN 56 57  
STRAND 58 65  
HELIX 69 74  
TURN 79 80  
STRAND 82 87  
TURN 93 94  
TURN 96 97  
HELIX 98 109  
STRAND 112 118  
HELIX 120 123  
HELIX 127 152  
HELIX 156 158  
STRAND 159 164  
TURN 165 166  
HELIX 177 180  
TURN 184 188  
STRAND 191 191  
STRAND 193 197  
TURN 200 202  
HELIX 211 215  
STRAND 222 225  
STRAND 229 229  
STRAND 237 241  
TURN 242 243  
TURN 249 251  
HELIX 261 265  
TURN 266 267  
HELIX 274 288  
TURN 290 291  
STRAND 294 294  
STRAND 296 297  
HELIX 301 305  
TURN 306 307  
TURN 314 315  
STRAND 319 319  
TURN 322 323  
HELIX 324 326  
TURN 328 331  
STRAND 336 340  
STRAND 351 361  
STRAND 364 374  
TURN 375 376  
STRAND 377 378  
STRAND 382 389  
STRAND 394 401  
TURN 408 417  
TURN 422 423  
STRAND 427 435  
TURN 437 438  
STRAND 441 445  
STRAND 450 450  
TURN 452 453  
STRAND 456 461  
SEQUENCE 461 AA; 50921 MW; 382F33F3CE446738 CRC64;  
43.9%; Score 1109; DB 1; Length 461;  
ry Match

Best Local Similarity 48.4%; Pred. No. 3.9e-84;  
Matches 226; Conservative 66; Mismatches 165; Indels 10; Gaps 9;  
QY 5 WIVAFIFGFSRQKVCYERLQCFKDLPTWTFSTELVGLPWSPEKINTRELLYTIHNP 64  
DB 1 WTLS-LLLGAVGVNEVCYERLQCFSDSPWAGIVERPLKILPWSPEKNTRELLYTNEP 59  
QY 65 NAYOEISAVNSSTIOASYGTDKITRINIAGW--KTDGKQEDMCNVLLQLEDINCINLD 122  
DB 60 DNFEIIVA-DPSTIQSSNENTGRKTRFIHGHIDGERSWLSTMCQNMFKVESVNCICVD 118  
QY 123 WINGSR-EYIHAVNLRVVGAEVAYFIDVLMKKFYSKVLHIGHSIHAHLAGEAGSRI 181  
DB 119 WKSGRATAYSQASQNVRIVGAEVAYLVGLQSPFSPSNVHIIIGHSLSHAAGEAGRRT 178  
QY 182 PG-LGRIITGLDPAGPEPHNTPKVEVRLDPSDANFVDVHTNAARILFELGVGTIDACGHL 240  
DB 179 NGAVGRITGLDPAEPCFQGTPELVRLDPSDAQFVDVHTDIAPFIPNLGFGMSQTAGHL 238  
QY 241 FYPNGGKHPGCCDLITPLLKFNFNAYKKEVASFFDCNHARSYQFYAESILNPDATAYP 300  
DB 239 FFPNGGKEMFGCKQNVLSQI-VDIDGIWQTRDPAACNHLRSYKYVYDLSILNPDGAFGS 297  
QY 301 CRSYTSFKAGNCFPCSKGECPTMCHPADRFHFKMKTNGSHYFLNTGSLSPPARWKL 360  
DB 298 CASYSDFTANKCFPCSGECGQMGHYADRFPGRT-KGVGQLFYLTNGDASNFARWRV 356  
QY 361 VKLSGSEVTQGTVFLRVGGAIGTGEFAIVSGKLEPGMTYTKLIDADVNVGNITSVOFIW 420  
DB 357 VTLSGKVT-GHVLVSLFGNKSQRQYEIFQGTLLKPDNTYSNEFSDSDEVDGDEKVKFIW 415  
QY 421 KXHLFEDSQKLGAEWINTSGKYKSTFCSQDINGENILQNKPC 467  
DB 416 YNNVINLTLPKVGASK-ITVERNDGVSFNFCSSETVRDVLTLTAC 461  
RESULT 10  
LIPP\_CAVPO  
ID\_LIPP\_CAVPO STANDARD; PRT; 465 AA.  
AC PS0903;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Triacylglycerol lipase, pancreatic precursor (EC 3.1.1.3) (Pancreatic  
lipase) (PL).  
GN PNLIP.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RX MEDLINE=94139898; PubMed=8307159;  
RA Carriere F., Thirstrup K., Hjorth S., Boel E.;  
RT "Cloning of the classical guinea pig pancreatic lipase and comparison  
with the lipase related protein 2";  
RL FEBS Lett. 338:63-68(1994).  
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
fatty acid anion.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
CC -1- SIMILARITY: Contains 1 PLAT domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X77403; CAA54585.1; -.  
DR

```

PIR; S41084; S41084.
HSP; P29183; 1HPL.
InterPro; IPR000734; Lipase.
InterPro; IPR001024; Lipoxigenase LH2.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF00151; lipase; 1.
Pfam; PF01477; PLAT; 1.
PRINTS; PRO0821; TAGLIPASE.
SMART; SM00308; LH2; 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Pancreas; Glycoprotein; Signal.
SIGNATURE 1 46
CHAIN 17 45
DOMAIN 355 465
ACT_SITE 169 193
ACT_SITE 193 193
ACT_SITE 280 280
DISULFID 20 26
DISULFID 107 118
DISULFID 254 278
DISULFID 302 313
DISULFID 316 321
DISULFID 449 465
CARBOHYD 351 351
CARBOHYD 398 398
CARBOHYD 425 425
SEQUENCE 465 AA; 51858 MW; CF3A26CB1A6C708 CRC64;

ry Match 43.8%; Score 1108; DB 1; Length 465;
t Local Similarity 47.8%; Pred. No. 4.8e-84;
ches 225; Conservative 72; Mismatches 164; Indels 10; Gaps 9;

1 MLGIVTAVFLPFGTSRGKEVCYERLCGFDGKLPWTRFSTELVGLPWSPEKINTRFLYLT 60
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1 MLLWALP-LLLGAVAGLEVYERLCGFGNRPWSGGTLERPFT---LPSTPKIVNTR 59
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

61 IHNPNAYQIBISAVNSSTIQASVFGDKTRINIAAG--KTDGKWDMCNVLLQLEDINC 118
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
60 NENPNYQRIIA-DSSVRSDDPKTRTRIIGHFDKGEENWLDCKALFQVESVNC 118
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

119 INLDWINGSRE-YIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHAGEA 177
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
119 ICVDWRGSGRTLYSQASQNIQVVGAEVAYLINFQSLDYPSPSVHIIHSLGSHAAGEA 178
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

178 GSRIPG-LGRITGLDPAGFPFHNTPKPEVRLDPSDANFVDVHTNAARILFELGVGTIDAC 236
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
179 GRTNGALGRITGLDPABEYFYQYFEIVRLDPSDAQFVDVHTDGNPIINLFGMSQTV 238
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

237 GHLDFYPNGKHMPCEDLIITPLAKFNFNAYKKEMAGFFDCNHARSQFYAESILNPDAF 296
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
239 GHLDFPFGGLQMPGCGKXNLSQI-VDIDGIWEGTRDFAACNHLRSKYKYSITNPKGF 297
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

297 IAYPCRSYTSFKAGNCFSCKEGCTWGHFADRFKPMKNTGSHVFLNTGSLSPFARWR 356
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
298 AGFSCDSYSSSSNNKCFPCATGECFQMGHYADKPPGKT-KENFQNFYLTNGDKSNFSRW 356
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

357 HKLSVKLSGSEVTOGTVPLRVGGAIGTKTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
357 YRIATVLSQKVT-GHVLVSLFGAGNTKQVEIYRGLSKPGNNHSNEISDVVDVGLQKV 415
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

417 QFIWKHFLPESQNLGAEVINTSGKYGKSTFCSDQIDNGPILQNLKPC 467
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
416 KEIWNVYNITLPRKVGASRITVRSR-GRVDFPCSDQTVREEVLLTLQPC 465
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

r 11
JIFS RABIT STANDARD; PRT; 465 AA.
302157;
11-JUL-1993 (Rel. 26, Created)
11-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)

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DE Triacylglycerol lipase, pancreatic precursor (EC 3.1.1.3) (Pancreatic lipase) (PL).

GN PNLIP.

OS Oryctolagus cuniculus (Rabbit).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_Taxid=9986;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=93075235; PubMed=1445366;

RA Aleman-Gomez J.A., Colwell N.S., Sasser T., Kumar V.B.;

RT "Molecular cloning and characterization of rabbit pancreatic

triglyceride lipase.";

RL Biochem. Biophys. Res. Commun. 188:964-971 (1992).

CC -|- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a

fatty acid anion.

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.

CC -|- SIMILARITY: Contains 1 PLAT domain.

CC -----

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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----

CC EMBL; M99365; AAA31489.1; --

DR HSP; P29183; 1HPL.

DR InterPro; IPR000734; Lipase.

DR InterPro; IPR001024; Lipoxigenase LH2.

DR InterPro; IPR000379; Ser\_estrs\_site.

DR Pfam; PF00151; lipase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PRO0821; TAGLIPASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00120; LIPASE\_SER; 1.

DR PROSITE; PS50095; PLAT; 1.

DR Hydrolase; Lipid degradation; Pancreas; Signal.

FT SIGNAL 1 16

FT CHAIN 17 465

FT DOMAIN 355 465

FT ACT\_SITE 170 170

FT ACT\_SITE 194 194

FT ACT\_SITE 281 281

FT DISULFID 20 26

FT DISULFID 108 119

FT DISULFID 255 279

FT DISULFID 303 314

FT DISULFID 317 321

FT DISULFID 449 465

FT SEQUENCE 465 AA; 51161 MW; 47F53275997BBA19 CRC64;

Query Match 43.7%; Score 1105; DB 1; Length 465;

Best Local Similarity 48.1%; Pred. No. 8.4e-84;

Matches 230; Conservative 74; Mismatches 150; Indels 24; Gaps 13;

QY 1 MLGIVTAVFLPFGTSRGKEVCYERLCGFDGKLPWT-----RTPSTELVGLPWSPEKINTR 55

DB 1 MLLWALP-LLLGAVAGLEVYERLCGFGNRPWSGGTLERPFT---LPSTPKIVNTR 55

QY 56 FLLYTNPNAYQIBISAVNSSTIQASVFGDKTRINIAAGWTKTDGK--WORDMCNVLLQL 113

DB 56 FLLYTNPNPNFOEISA-DASTIRGNSFRTRDKTRTRIIGHFDKGEENWLSNLCENLFQV 114

QY 114 EDINCINLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAH 172

DB 115 ETVNCICVDWKSGSRTTYQATQNIIRVGAEVAYLVGTQLQSLGYSPPSNIHVIGHSLGAH 174

QY 173 LAGEAGSRIPG-LGRITGLDPAGFPFHNTPKPEVRLDPSDANFVDVHTNAARILFELGVG 231

DB 175 AAGEVGRNTGTRITGLDPAEYFYQYFEIVRLDPSDAQFVDVHTDPAWPNLPGF 234

232 TIDAGHLDFVPGCKHMPGCEDELITPLKFNPNAYKKEVAFDCNCHARSYQVFAESIL 291  
 235 MSQTVGLHDFPFNGKEMPGCKQKVLUSQI-VDINGVWEGTRDFVACNHLRSYKYVADSI 293  
 292 NPDAFIAPYCRSYTSFKAGNCGFCSCGEGCPTMGHAFDRHFKNMKTN--GSHVFLNTGSL 349  
 294 NPNGFAGFSCASYTAFSANKCFPCS-NGCFQMGHYADRF---SRKTDGVGTFFYLNKGD 349  
 350 SPFAEMHKLVSXKLSGSEVTCGTGTVFLVGAIGAKTGEPAIVSGKLEBPGMYTYKLLDADVN 409  
 350 SNFARWYQVAVTLUSGRVTF-GHVLVSLYSGKNSKQYEIFTGLLKPQTHLNEFDSVD 408  
 410 VGNITSVQVFWKHLFEDSQNKLAENAVINTSGYGVKSPQSDIMGNILQNLKPC 467  
 409 VGDYQVKFVWYNNVNTPLPKVGASQ-ITVEQNDGRVFKFCSTDVREDILLITLTPC 465

JT 12  
 -MOUSE  
 -LIP2\_MOUSE STANDARD; PRT; 468 AA.  
 P17892;  
 01-NOV-1990 (Rel. 16, Created)  
 01-NOV-1990 (Rel. 16, Last sequence update)  
 15-SEP-2003 (Rel. 42, Last annotation update)  
 Pancreatic lipase related protein 2 precursor (EC 3.1.1.3) (Cytotoxic  
 T lymphocyte lipase).  
 PNLIPR2 OR PLRP2.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=T-cell;  
 MEDLINE=90150272; PubMed=2302735;  
 Grusby M.J., Nabavi N., Wong H., Dick R.F., Bluestone J.A.,  
 Schotz M.C., Glimcher L.H.,  
 "Cloning of an interleukin-4 inducible gene from cytotoxic T  
 lymphocytes and its identification as a lipase,"  
 Cell 60:451-459(1990).  
 -!- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN CYTOTOXIC T LYMPHOCYTE  
 (CTL) EFFECTOR FUNCTION.  
 -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
 fatty acid anion.  
 -!- INDUCTION: By interleukin-4.  
 -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
 -!- SIMILARITY: Contains 1 PLAT domain.

-----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----

EMBL; M30687; AAA37491.1; ALT\_INIT.  
 HSSP; P54318; 1BU8.  
 MGD; MGI:1336202; Pnlipr2.  
 GO; GO:0006968; P:cellular defense response; IMP.  
 GO; GO:0007586; P:digestion; IMP.  
 InterPro; IPR000734; Lipase.  
 InterPro; IPR001024; Lipoxigenase\_LH2.  
 InterPro; IPR000379; Ser esterase.  
 Pfam; PF00151; lipase; 1.  
 Pfam; PF01477; PLAT; 1.  
 PRINTS; PR00821; TAGLIPASE.  
 SMART; SMO0308; LH2; 1.  
 PROSITE; PS00120; LIPASE\_SER; FALSE\_NEG.  
 PROSITE; PS00095; PLAT; 1.  
 Hydrolase; lipid degradation; Pancreas; Glycoprotein; Signal.  
 SIGNAL 16  
 [2]

FT CHAIN 17 468 PANCREATIC LIPASE RELATED PROTEIN 2.  
 FT DOMAIN 356 468 PLAT.  
 FT ACT\_SITE 170 170 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 194 194 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 281 281 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 20 26 BY SIMILARITY.  
 FT DISULFID 108 119 BY SIMILARITY.  
 FT DISULFID 255 279 BY SIMILARITY.  
 FT DISULFID 303 314 BY SIMILARITY.  
 FT DISULFID 452 468 BY SIMILARITY.  
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 468 AA; 52585 MW; 1698E35C0F4E1534 CRC64;  
 Query Match 43.3%; Score 1094.5; DB 1; Length 468;  
 Best Local Similarity 46.7%; Pred. No. 6.3e-83;  
 Matches 220; Conservative 68; Mismatches 176; Indels 7; Gaps 6;  
 Qy 1 MLGIMIVAFLEFSGRGKEVCYERLGCFCFSGDGLPWTTRTFSTELVGLPFWSPKINRFLIYT 60  
 Db 1 MLLCWLVS-LLLATVGGKEVCYHGLGFCFSGNDKPMAGMIQRPSKIFPWSPEIDIRFLIYT 59  
 Qy 61 IHNPNAYOISAVNSTTICASYFTGDKITRINIAKWTGDK--WORDMNCVLLQLEDINC 118  
 Db 60 NENPNYQIISATDPATINASFQDRKTRFIHGFIDKBEGMLLDCKCFQVEKVCNC 119  
 Qy 119 INLDWINGSR-EYIHAVNNLRVVGAEVAFIDVLMKPEYSPKVHLIGHSLGAHAGEA 177  
 Db 120 ICVDWKRGSRTEYQTASYNTRVLGAEIAFLVQLSTENGYSFENVHLIPHLSGSHVAGEA 179  
 Qy 178 GSRIPG-LGRIITGLDPAGFFHNTPEKVRLPDSANFVDVHTNAARILBELGVGTIDAC 236  
 Db 180 GRLEGHVGRITGLDPAEPFCQGLPEEVRLPDSAMFVDVHTDSAPIPYLGFQMSQKV 239  
 Qy 237 GHLDFYPNGCKEMPGCEDLITELLKFNFNAYKKEVAFDCNCHARSYQVFAESILNPDAP 296  
 Db 240 GHLDFYPNGCKEIPGCKNLSIT-VDINGWEGTRNPAACHLRSYKYVASSILNPDGP 298  
 Qy 297 IAYPCSYTSFKAGNCGFCSCGEGCPTMGHAFDRHFKNMKTNGSHYFLNTGSLSPFARWR 356  
 Db 299 LGYPCSSYFKFQHNDCFFSPGECQKMGHYADFEKGT-ATVEQTFELNTADTGNFTWR 357  
 Qy 357 HKLSVKLSSEVTCGTGTVFLRVGAIGAKTGEPAIVSGKLEBPGMYTYKLLDADVNYGNTSV 416  
 Db 358 YKVSVTLSGPKLSGLVILVAGCNANSKQYEVFKGSLQPEARYIRIDVDVNVGEIQKV 417  
 Qy 417 QFIWKHKLFPEDSQNKLAENAVINTSGYGVKSPQSDIMGNILQNLKPC 467  
 Db 418 KFLWNNKVINLFRPTMGASQITLQRAKDGKBFNCTSNVHEDVLQSLYPC 468

RESULT 13  
 LIPP\_RAT STANDARD; PRT; 465 AA.  
 ID LIPP\_RAT AC P27657;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Triacylglycerol lipase, pancreatic precursor (EC 3.1.1.3) (Pancreatic  
 lipase) (PL).  
 GN PNLIP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94262798; PubMed=8203536;  
 RA Payne R.M., Sims H.F., Jennens M.L., Lowe M.E.;  
 RT "rat pancreatic lipase and two related proteins: enzymatic properties  
 and mRNA expression during development";  
 RL Am. J. Physiol. 266:G914-G921(1994).  
 [2]

SEQUENCE FROM N.A., AND SEQUENCE OF 17-37.  
 STRAIN=Sprague-Dawley; TISSUE=Pancreas;  
 MEDLINE=93252914; PubMed=8486693;  
 Wilschut M.J., Andrews P.C., Nichols R., Blevins G.T. Jr.,  
 Logsdon C.D., Williams J.A.,  
 "Identification and cloning of GP-3 from rat pancreatic acinar  
 zymogen granules as a glycosylated membrane-associated lipase";  
 J. Biol. Chem. 268:10303-10311(1993).  
 -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN FAT METABOLISM. IT  
 PREFERENTIALLY SPLITS THE ESTERS OF LONG-CHAIN FATTY ACIDS AT  
 POSITIONS 1 AND 3, PRODUCING MAINLY 2-MONOACYLGLYCEROL AND FREE  
 FATTY ACIDS, AND SHOWS CONSIDERABLY HIGHER ACTIVITY AGAINST  
 INSOLUBLE EMULSIFIED SUBSTRATES THAN AGAINST SOLUBLE ONES.  
 -!- CATALYTIC ACTIVITY: Triacylglycerol + H<sub>2</sub>O = diacylglycerol + a  
 fatty acid anion.  
 -!- SUBCELLULAR LOCATION: Secreted.  
 -!- TISSUE SPECIFICITY: PANCREAS. PANCREATIC SECRETORY (ZYMOGEN)  
 GRANULE.  
 -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
 -!- SIMILARITY: Contains 1 PLAT domain.

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EMBL; M58369; AA79888.1; ..  
 HSSP; P00591; 1ETH.  
 InterPro: IPR000734; Lipase.  
 InterPro: IPR001024; Lipoxigenase LH2.  
 InterPro: IPR000379; Ser\_estrs\_site.  
 Pfam; PF00151; lipase; 1.  
 Pfam; PF01477; PLAT; 1.  
 PRINTS; PRO0821; TAGLIPASE.  
 SMART; SM00308; LH2; 1.  
 PROSITE; PS00120; LIPASE SER; 1.  
 PROSITE; PS00095; PLAT; 1.  
 Hydrolase; Lipid degradation; Pancreas; Signal.  
 SIGNAL 1 16  
 CHAIN 17 465 TRIACYLGLYCEROL LIPASE, PANCREATIC.  
 DOMAIN 355 465 PLAT.  
 ACT\_SITE 169 169 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 ACT\_SITE 193 193 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 ACT\_SITE 280 280 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 DISULFID 20 26 BY SIMILARITY.  
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ty Match 42.5%; Score 1073; DB 1; Length 465;  
 - Local similarity 46.1%; Pred. No. 3.7e-81;  
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 1 MMLMTFAVL-LGAVAGKEVCFDKLGGCFDDPWSGTIDRLPKALPSPAQINTRFLVLT 59  
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 60 NENQDNQKITS-DASSIRNSFNKTRNKRTRIIHGFIDKGEENWLSMDCKMFKVESVNC 118  
 119 INLDWINGSR-EYHAVNNLVYGAEVAFIDVLKKFSPKVLHIGSLGHAHAGEA 177  
 119 ICVDWKGSGRATYQATQNVWVGAEVALLVNLKSLDGLGHPDPNVHLIGHSLGSHVAGEA 178  
 178 GSRIPG-LGRITGLDPAQFPFFHPKPEVRLDPSDANFVDVHTNARILFELGVGTIDAC 236

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 Db 298 SGFSCSSYNVFSANKFCGSEGGCPQMGHYADKYPGKT-KELYOKFVLNTGDKSNFARWR 356  
 QY 357 HKLSVKLSGSEVTOGTFLRVGGAGTKGTGPAIVSGKLEPMTYTKLIDADVNVGNITSV 416  
 Db 357 YQVTVTLSGQKVT-GHILVSLFNGNGSKQYEVFKGSLHPGDTHVKEFDSMDVDGLQKV 415  
 QY 417 QPIWKKHLFEDSQNKLGAEMVINTSGKYGKSTFCSDINGPNILQNLKPC 467  
 Db 416 KEIYNVNTPLFKVGSR-ISVERNDGRVFNFCSDQTVREDVILLTSLAC 465

RESULT 14  
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 ID LIPP\_PIG STANDARD; PRT; 450 AA.  
 AC P00591;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Triacylglycerol lipase, pancreatic (EC 3.1.1.3) (Pancreatic lipase)  
 DE (PL)  
 GN PNLIP.  
 OS Sus scrofa (Pig)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE OF 308-449.  
 RX MEDLINE=82113655; PubMed=7326260;  
 RA de Caro J.D., Boudouard M., Bonicel J.J., Guidoni A.A., Desnuelle P.,  
 Roverly M.;  
 RA "Porcine pancreatic lipase. Completion of the primary structure";  
 RT Biochim. Biophys. Acta 671:129-138(1981).  
 RN [2]  
 RP SEQUENCE OF 1-234, AND CARBOHYDRATE-LINKAGE SITE.  
 RX MEDLINE=79236335; PubMed=380992;  
 RA Bianchetti J.D., Bidaud J., Guidoni A.A., Bonicel J.J., Roverly M.;  
 RT "Porcine pancreatic lipase. Sequence of the first 234 amino acids of  
 the peptide chain";  
 RL Eur. J. Biochem. 97:395-405(1979).  
 RN [3]  
 RP SEQUENCE OF 235-307.  
 RX MEDLINE=80088446; PubMed=518929;  
 RA Guidoni A.A., Bonicel J.J., Bianchetti J.D., Roverly M.;  
 RT "Porcine pancreatic lipase. Sequence between the 235th and 307th  
 amino acids";  
 RL Biochimie 61:841-845(1979).  
 RN [4]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=83105095; PubMed=7151781;  
 RA Benkhoukha F., Guidoni A.A., de Caro J.D., Bonicel J.J.,  
 Desnuelle P.A., Roverly M.;  
 RT "Porcine pancreatic lipase. The disulfide bridges and the sulfhydryl  
 groups";  
 RL Eur. J. Biochem. 128:331-341(1982).  
 RN [5]  
 RP SUBSTRATE-BINDING SITE.  
 RX MEDLINE=82000578; PubMed=6791692;  
 RA Guidoni A.A., Benkhoukha F., de Caro J.D., Roverly M.;  
 RT "Characterization of the serine reacting with diethyl p-nitrophenyl  
 phosphate in porcine pancreatic lipase";  
 RL Biochim. Biophys. Acta 660:148-150(1981).  
 RN [6]  
 RP STRUCTURE OF CARBOHYDRATE.  
 RX MEDLINE=88082841; PubMed=3691527;  
 RA Fournet B., Leroy Y., Montreuil J., Decaro J., Roverly M.,

van Kuik J.A., Vliegthart J.F.G.;  
"Primary structure of the glycans of porcine pancreatic lipase.";  
Eur. J. Biochem. 170:369-371(1987).  
[7]  
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS TO 30-32.  
MEDLINE=98273347; PubMed=8663362;  
Hermoso J., Pignol D., Kerfelec B., Crenon I., Chapus C.,  
Fontecilla-Camps J.C.;  
"Lipase activation by nonionic detergents. The crystal structure of  
the porcine lipase-colipase-tetraethylene glycol monoethyl ether  
complex.";  
J. Biol. Chem. 271:18007-18016(1996).  
-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
fatty acid anion.  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
-!- SIMILARITY: Contains 1 PLAT domain.  
-!- DATABASE: NAME=Worthington enzyme manual;  
WWW="http://www.worthington-biochem.com/manual/L/Pl.html".  
PDB; IETH, 07-DEC-96.  
InterPro; IPR000734; Lipase.  
InterPro; IPR001024; lipoxigenase LH2.  
InterPro; IPR000379; Ser esters\_site.  
Pfam; PF00151; lipase; 1.  
Pfam; PF01477; PLAT; 1.  
PRINTS; PR00821; TAGLIPASE.  
SMART; SM00306; LH2; 1.  
PROSITE; PS00120; LIPASE\_SER; 1.  
PROSITE; PS00095; PLAT; 1.  
Hydrolase; Lipid degradation; Pancreas; Glycoprotein; 3D-structure.  
DOMAIN 339 450  
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ACT\_SITE 177 177 CHARGE RELAY SYSTEM.  
ACT\_SITE 264 264 CHARGE RELAY SYSTEM.  
DISULFID 4 10  
DISULFID 91 102 IN ISOMER 1.  
DISULFID 91 104 IN ISOMER 2.  
DISULFID 238 262  
DISULFID 286 297  
DISULFID 300 305  
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19 EVCYERLCGKGLPWTRTFSTELVGLPWSPEKINTFLFYTHNPAYQISAVNSSTI 78  
2 EVCPPRLGCFSDAPWAGIVQREPLKLPSPKXVDTRFLYTNQNNYQELVA-DPSTI 60  
79 QASYEGGDKITRINIAGW--KTGKQWRDMCNVQLQLEPINCINLDWNGRE-YIHAVN 135  
61 TNSNFRMDKTRIFIHGFDKGDWLSNCKNLFKVESVNCICVDWGGERTGYTQASQ 120  
136 NLRVGAEVAFYIDVLMKKEFYSPKSVHLIGHSLGAHLAGEAGSRIPG-LGRITGLDPAG 194  
121 NIRVGAEVAFYEVVLKSLGYSFSPNVHIGSLGSHAGEAGRTNGTIERITGLDPAE 180  
195 PFPHNTPEVRLDPSDANFVDVHTVAAILFELGVGTTIDACGHLDFYNGGKMPGCCD 254  
181 PCFGTPELVRLDPSDAKFVDVHTDAAPILFNLGFGMSQTVGHLDFFPNGKQMPGCCQ 240  
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241 NILSQI-VDIDGIEWGTRDPAVACHLRSYKYVADSLINDPGAPGFCDSYVFTANKCF 299  
315 CSKEGCTMGHFADRPHKMKMTNG--SHYFNTGSLSPFARWRKLSVLSGSEVTQGT 372  
300 CPSEGGCPQMGHYADRF---PGKTINGVSQVFLNTGASNFAWRKVSVTLGSKVVT-GH 355  
373 VFLRVGGAIGKTEFAIVSGKLEPGMGTYYTKLIDADVNVGNITSVQFIW-KKHLFEDSQNK 431

356 ILVSLFGNEGSRQVEIYKGTLPDNTHTSDREDSVDEVDLQKVFYNNVNTPLPR 415  
432 LGAEWINTSGKYGYKSTFCSDQDIMPNGNILQNLKPC 467  
416 VGASK-ITVERNDGKYDFCSQETVREEVLLTNPC 450  
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LIPH HUMAN STANDARD; PRT; 499 AA.  
ID LIPH HUMAN STANDARD; PRT; 499 AA.  
AC P1150; P78529; Q99465;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Triacylglycerol lipase, hepatic precursor (BC 3.1.1.3) (Hepatic  
lipase) (HL).  
GN LIPC OR HTGL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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RC TISSUE=Liver;  
RX MEDLINE=88273217; PubMed=2839510;  
RA Martin G.A., Busch S.J., Meredith G.D., Cardin A.D., Blankenship D.T.,  
Mao S.J.T., Rehtin A.E., Woods C.W., Racke M.M., Schafer M.P.,  
Fitzgerald M.C., Burke D.M., Flanagan M.A., Jackson R.L.;  
RT "Isolation and cDNA sequence of human postheparin plasma hepatic  
triglyceride lipase.";  
RL J. Biol. Chem. 263:10907-10914(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=88112595; PubMed=2828141;  
RA Stahnke G., Sprengel R., Augustin J., Will H.;  
RT "Human hepatic triglyceride lipase: cDNA cloning, amino acid sequence  
and expression in a cultured cell line.";  
RL Differentiation 35:45-52(1987).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=88087233; PubMed=2447084;  
RA Datta S., Luo C.C., Li W.H., Vantuinen P., Ledbetter D.H., Brown M.A.,  
Chen S.H., Liu S., Chan L.;  
RT "Human hepatic lipase. Cloned cDNA sequence, restriction fragment  
length polymorphisms, chromosomal localization, and evolutionary  
relationships with lipoprotein lipase and pancreatic lipase.";  
RL J. Biol. Chem. 263:1107-1110(1988).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90105435; PubMed=2805236;  
RA Cai S.J., Wong D.M., Chen S.H., Chan L.;  
RT "Structure of the human hepatic triglyceride lipase gene.";  
RL Biochemistry 28:8966-8971(1989).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90216670; PubMed=2324091;  
RA Ameis D., Stahnke G., Kobayashi J., McLean J., Lee G., Buscher M.,  
Schotz M.C., Will H.;  
RT "Isolation and characterization of the human hepatic lipase gene.";  
RL J. Biol. Chem. 265:6552-6555(1990).  
RN [6]  
RP SEQUENCE OF 464-499 FROM N.A.  
RX MEDLINE=97018564; PubMed=8865180;  
RA Takagi A., Ikeda Y., Mori A., Ashida Y., Yamamoto A.;  
RT "Identification of a BcNI polymorphism in exon 9 of the human  
hepatic triglyceride lipase gene.";  
RL Mol. Cell. Probes 10:313-314(1996).  
RN [7]  
RP VARIANTS PHE-289 AND MET-405.  
RX MEDLINE=93250827; PubMed=1301939;

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395 ASNTYSLITLDVDIGELIMIXFKWENSANWANDTVQTIIPNSTGPRHSGVLKTIR 454

441 --SGKYGYKSTFCSD 454

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455 VKAGETQORMTFCSEN 470

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:ime : 20 secs



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number of hits satisfying chosen parameters: 1139956

um DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2.6/prodata/2/ina/6A-COMB.seq.\*
- 4: /cgn2.6/prodata/2/ina/6B-COMB.seq.\*
- 5: /cgn2.6/prodata/2/ina/PCUTUS-COMB.seq.\*
- 6: /cgn2.6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Query Match %	Length	DB	ID	Description
1	1402.4	99.9	2352	4	US-09-411-132A-1	Sequence 1, Appli
2	1399.4	99.7	1401	4	US-09-411-132A-2	Sequence 2, Appli
3	74.6	5.3	1035	4	US-08-985-492-9	Sequence 9, Appli
4	74.6	5.3	1065	4	US-08-985-492-5	Sequence 5, Appli
5	74.6	5.3	1382	4	US-08-985-492-3	Sequence 3, Appli
6	74.6	5.3	2565	4	US-08-985-492-7	Sequence 7, Appli
7	45.2	3.2	1048	4	US-09-166-205B-63	Sequence 62, Appli
8	43.4	3.1	1341	1	US-08-180-209B-26	Sequence 26, Appli
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3	43.4	3.1	1341	5	PCT-US94-02629-26	Sequence 26, Appli
4	39.2	2.8	8920	2	US-08-446-855A-1	Sequence 1, Appli
5	39.2	2.8	8920	3	US-09-150-741-1	Sequence 1, Appli
6	39.2	2.8	1664976	4	US-08-916-421B-1	Sequence 1, Appli
7	37.2	2.6	231	3	US-08-905-124-4	Sequence 4, Appli
8	37.2	2.6	9734	3	US-09-347-114A-80	Sequence 80, Appli
9	36	2.6	3832	4	US-08-961-527-92	Sequence 92, Appli
0	35.6	2.5	2341	3	US-08-714-918-102	Sequence 102, App
1	35.6	2.5	2341	3	US-09-265-315-102	Sequence 102, App
2	35.6	2.5	2341	3	US-09-265-315-102	Sequence 102, App
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Sequence 14, Appli  
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Sequence 40, Appli

ALIGNMENTS

RESULT 1

US-09-411-132A-1  
; Sequence 1, Application US/09411132A  
; Patent No. 6558936

GENERAL INFORMATION:

APPLICANT: Khodadoust, Mehran

APPLICANT: Kapeller-Libermann, Rosana

TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding  
TITLE OF INVENTION: Them and uses of Both of these

FILE REFERENCE: 1014-14

CURRENT APPLICATION NUMBER: US/09/411,132A

CURRENT FILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn ver. 2.1

SEQ ID NO 1

LENGTH: 2352

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure

LOCATION: (2159)

NAME/KEY: unsure

LOCATION: (2307)

NAME/KEY: unsure

LOCATION: (2313)

US-09-411-132A-1

Query Match 99.9%; Score 1402.4; DB 4; Length 2352;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1403; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 125 ATGCTTGAATTTGGATTGTCATTTCTTTTGGACATCAAGAGAAAGAGTT 184

QY 61 TCGTATGAAGGTTAGGGTGTTCACAGATGTTTACCATGGACCGAGCTTTCTCAACA 120

Db 185 TCGTATGAAGGTTAGGGTGTTCACAGATGTTTACCATGGACCGAGCTTTCTCAACA 244

QY 121 GAGTTGGTAGGTTTACCTGGTCTCCAGAGAGATAAACACTCGTTTCTGCTTACACT 180

Db 245 GAGTTGGTAGGTTTACCTGGTCTCCAGAGAGATAAACACTCGTTTCTGCTTACACT 304

QY 181 ATACATCCCAATGCCCTATCAGAGATCAGTCGGTAACTTCTCAACTCCAGACC 240

Db 305 ATACATCCCAATGCCCTATCAGAGATCAGTCGGTAACTTCTCAACTCCAGACC 364

QY 241 TCATATTTTGAACACAGACAGATCACCGGTATCAACATAGCTGGATGAAACAGATGCC 300

Db 365 TCATATTTTGAACACAGACAGATCACCGGTATCAACATAGCTGGATGAAACAGATGCC 424

301 AAATGGCAGAGACATGTGCAATGTCTTCTACAGCTGGAAGATATAAATTCATTAAT 360  
425 AAATGGCAGAGACATGTGCAATGTCTTCTACAGCTGGAAGATATAAATTCATTAAT 484  
361 TTAGATTGGATCAACGGTTCACGGGAATACATCCATGCTGTAAACAATCTCGTGTGTT 420  
485 TTAGATTGGATCAACGGTTCACGGGAATACATCCATGCTGTAAACAATCTCGTGTGTT 544  
421 GGTGCTGAGTGGCTTATTTTATGATGTTCTCATGAAAAAATTTGAATATTCCTCTCT 480  
545 GGTGCTGAGTGGCTTATTTTATGATGTTCTCATGAAAAAATTTGAATATTCCTCTCT 604  
481 AAATGACATTTGATGGCCACAGCTTGGAGACACCTGCTGGGGAAGCTGGTCAAGG 540  
605 AAATGACATTTGATGGCCACAGCTTGGAGACACCTGCTGGGGAAGCTGGTCAAGG 664  
541 ATACAGGCTTGAAGAATAACTGGGTGGAGCCAGCTGGGCCATTTTCCACAACACT 600  
665 ATACAGGCTTGAAGAATAACTGGGTGGAGCCAGCTGGGCCATTTTCCACAACACT 724  
601 CCAAGGAAGTCAGGCTAGACCCCTCGATGCCAACTTTGTTGACGTTATTATACAAAT 660  
725 CCAAGGAAGTCAGGCTAGACCCCTCGATGCCAACTTTGTTGACGTTATTATACAAAT 784  
661 GCAGCTGCATCTCTTTGAGCTTGGTGGTGGACCATTTGATGCTGTGCTCATCTGAC 720  
785 GCAGCTGCATCTCTTTGAGCTTGGTGGTGGACCATTTGATGCTGTGCTCATCTGAC 844  
721 TTTTACCAATGAGGGAAGCACATGCCAGGATGTGAAGACTTAATTACACCTTTACTG 780  
845 TTTTACCAATGAGGGAAGCACATGCCAGGATGTGAAGACTTAATTACACCTTTACTG 904  
781 AAATTTAACTCAATGTTTACAAAAGAAATGGCTTCTTTGACGTGAACATGCC 840  
905 AAATTTAACTCAATGTTTACAAAAGAAATGGCTTCTTTGACGTGAACATGCC 964  
841 CGAAGTTATCAATTTTATGCTGAAAGCAATCTTAATCCCTGATGCAATTTATGCTATCT 900  
965 CGAAGTTATCAATTTTATGCTGAAAGCAATCTTAATCCCTGATGCAATTTATGCTATCT 1024  
901 TGTAGATCTTACACATCTTTTAAAGCAGGAAATGGCTTTTGTTCCTTCCAAAAGAGTTGC 960  
1025 TGTAGATCTTACACATCTTTTAAAGCAGGAAATGGCTTTTGTTCCTTCCAAAAGAGTTGC 1084  
961 CCAACAATGGGTCAATTTTGTGTGATAGATTTCACTTCAAAAATATGAAGACTTAATGATCA 1020  
1085 CCAACAATGGGTCAATTTTGTGTGATAGATTTCACTTCAAAAATATGAAGACTTAATGATCA 1144  
1021 CATTAATTTTAAACACAGGGTCCCTTTTCCCATTTGCGCGTTGGAGGCACAAATTTGCT 1080  
1145 CATTAATTTTAAACACAGGGTCCCTTTTCCCATTTGCGCGTTGGAGGCACAAATTTGCT 1204  
1081 GTTAACTCAGTGAAGCAAGTCACTCAAGGACTGTCTTTCTTCTGCTGAGCGGGCA 1140  
1205 GTTAACTCAGTGAAGCAAGTCACTCAAGGACTGTCTTTCTTCTGCTGAGCGGGCA 1264  
1141 ATTGGGAAAACCTGGGAGTTTGCATTTGTCAGTGGAAAACCTTGAGCCAGGCATGACTTAC 1200  
1265 ATTGGGAAAACCTGGGAGTTTGCATTTGTCAGTGGAAAACCTTGAGCCAGGCATGACTTAC 1324  
1201 ACAAAATTAATCGATGAGATGTTAACTGTTGGAACATTAACAAGTTCAGTTCATCTGG 1260  
1325 ACAAAATTAATCGATGAGATGTTAACTGTTGGAACATTAACAAGTTCAGTTCATCTGG 1384  
1261 AAAAAACATTTGTTTGAAGATTTCTCAGAAATAAGTTGGAGCAAAATGTTGATAAATACA 1320  
1385 AAAAAACATTTGTTTGAAGATTTCTCAGAAATAAGTTGGAGCAAAATGTTGATAAATACA 1444  
1321 TCTGGAAAATGAGATATAAATCTACCTTCTGTAGCCAGACATTAATGAGGACCTTAATTT 1380  
1445 TCTGGAAAATGAGATATAAATCTACCTTCTGTAGCCAGACATTAATGAGGACCTTAATTT 1504

Qy 1381 CTCAGAACTGAAACCATGCTAA 1404  
Db 1505 CTCAGAACTGAAACCATGCTAA 1528

## RESULT 2

US-09-411-132A-2  
; Sequence 2, Application US/09411132A  
; Patent No. 6558936  
; GENERAL INFORMATION:  
; APPLICANT: Khodadoust, Mehran  
; TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding  
; TITLE OF INVENTION: Them, and Uses of Both of These  
; FILE REFERENCE: 10147-14  
; CURRENT APPLICATION NUMBER: US/09/411,132A  
; CURRENT FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1401  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-411-132A-2

Query Match 99.7%; Score 1399.4; DB 4; Length 1401;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGGAAATTTGGATTGTTGCAATTCCTTTTGGCACATCAAGAGGAAAAAGAGTT 60  
Db 1 ATGCTTGGAAATTTGGATTGTTGCAATTCCTTTTGGCACATCAAGAGGAAAAAGAGTT 60  
Qy 61 TGTATGAAAGTTAGGTGTTTCAAAGATGTTTACCATGACGAGACTTCTCAACA 120  
Db 61 TGTATGAAAGTTAGGTGTTTCAAAGATGTTTACCATGACGAGACTTCTCAACA 120  
Qy 121 GAGTTGGTGGTGTACCTGGTCTCCAGAGAGATAAACAACACTCGCTTCTCTACT 180  
Db 121 GAGTTGGTGGTGTACCTGGTCTCCAGAGAGATAAACAACACTCGCTTCTCTACT 180  
Qy 181 ATACACAATCCCAATGCCCTATCAGGAGATCAGTGGGTTAAATTTCTTCAACTATCAAGCC 240  
Db 181 ATACACAATCCCAATGCCCTATCAGGAGATCAGTGGGTTAAATTTCTTCAACTATCAAGCC 240  
Qy 241 TCATATTTTGGAAACACAGCAAGATCACCGTATCAACATAGCTGGATGGAACACAGATGGC 300  
Db 241 TCATATTTTGGAAACACAGCAAGATCACCGTATCAACATAGCTGGATGGAACACAGATGGC 300  
Qy 301 AAATGSCAGAGACATGTGCAATGTGTTGTCTACAGCTGGAAGATATAAATTCATTAAT 360  
Db 301 AAATGSCAGAGACATGTGCAATGTGTTGTCTACAGCTGGAAGATATAAATTCATTAAT 360  
Qy 361 TTAGATTGGATCAACGGTTCACGGGAATACATCCATGCTGTAAACAATCTCCGTGTGTT 420  
Db 361 TTAGATTGGATCAACGGTTCACGGGAATACATCCATGCTGTAAACAATCTCCGTGTGTT 420  
Qy 421 GGTGCTGAGTGGCTTATTTTATGATGTTCTCATGAAAAAATTTGAATATTCCTCTCT 480  
Db 421 GGTGCTGAGTGGCTTATTTTATGATGTTCTCATGAAAAAATTTGAATATTCCTCTCT 480  
Qy 481 AAATGTCATCTGATTTGGCCACAGCTTGGAGCACACCTGGCTGGGGAAGCTGGGTCAAGG 540  
Db 481 AAATGTCATCTGATTTGGCCACAGCTTGGAGCACACCTGGCTGGGGAAGCTGGGTCAAGG 540  
Qy 541 ATACCAAGGCTTGGAAAGATAAATCGGTTGGAACCCAGCTGGGCCATTTTCCACAACACT 600  
Db 541 ATACCAAGGCTTGGAAAGATAAATCGGTTGGAACCCAGCTGGGCCATTTTCCACAACACT 600  
Qy 601 CCAAGGAAGTCAAGGCTAGACCCCTCGGATGCAACTTTGTTGACGTTATTATCATACAAAT 660  
Db 601 CCAAGGAAGTCAAGGCTAGACCCCTCGGATGCAACTTTGTTGACGTTATTATCATACAAAT 660



APPLICANT: South, Victoria J.  
 TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
 TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
 TITLE OF INVENTION: IN ENZYMAIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 STREET: 500 Arcola Rd. 3C43  
 CITY: Collegeville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,492  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fehner Ph.D., Paul F.  
 REGISTRATION NUMBER: 35,135  
 REFERENCE/DOCKET NUMBER: A2582-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610)454-3839  
 TELEFAX: (610)454-3808  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1065 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1065  
 8-985-492-5

ery Match 5.3%; Score 74.6; DB 4; Length 1065;  
 st Local Similarity 53.9%; Pred. No. 4.1e-13;  
 tches 202; Conservative 0; Mismatches 164; Indels 9; Gaps 2;  
 388 TACATCCATGCTGTAACAAATCTCCGTTGTTGGTCTGAGGTGCTTATTTATTTGAT 447  
 391 TACACGGATCGGTCATATATACAGGGTGTGGACACAGCAATGCCAGGATGCTCGAC 450  
 448 GTTCTCATGAAAAAATTGAATATTCCTCTTAAAGTGCACTTGATTTGCCACAGCTTG 507  
 451 TGGCTGCAGGAGAGGACGATTTTCTCTCGGAATGTCACATGATCGCTACAGCCTC 510  
 508 GGAGCACACCTGGCTGGGAGCTGG--GTCAGGATACCGGCTTGGAGAGTAATCT 564  
 511 GGAGCGCACGTGGCGGGTATGAGGCAATCTCGTGAAGGAACGCTGGCGCGAATCACA 570  
 565 GGGTTGACCCAGCTGGGCGCATTTTCCACACACTCCAAAGGAAGTCAGGCTAGACCCC 624  
 571 GGTTTGGATCTCGCGGCGCCATGTTTGAAGGGCGGACATCCACAGAGGCTCTCTCG 630  
 625 TCGGATGCCAATTTTGTGAGCTTATTCATAAATGCAAGTCCGATCTCTTTGAGCTT 684  
 631 GACGATGCAGATTTTGTGAGTGTCTCCACACCTACACCGGTTCTCTCGGTTGAGCAT 690  
 685 GGTGTGGAACCAATTGATGCTGTGGTTCATCTTACCTTTTACCCAAATGGAGGAGCAC 744  
 691 GGTATTCAGA-----TGCCTGTGGGCGACATTCACATCTACCCCAATGGGGGTGACTTC 744  
 745 ATGCCAGATGTGAA 759  
 745 CAGCAGGCTGTGA 759

## RESULT 5

US-08-985-492-3  
 ; Sequence 3, Application US/08985492  
 ; Patent No. 6395530  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jaye, Michael C.  
 ; APPLICANT: Doan, Kim-Anh T.  
 ; APPLICANT: Krawiec, John A.  
 ; APPLICANT: Lynch, Kevin J.  
 ; APPLICANT: Amin, Dilip V.  
 ; APPLICANT: South, Victoria J.  
 ; TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL  
 ; TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE  
 ; TITLE OF INVENTION: IN ENZYMAIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 ; STREET: 500 Arcola Rd. 3C43  
 ; CITY: Collegeville  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19426  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/985,492  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fehner Ph.D., Paul F.  
 ; REGISTRATION NUMBER: 35,135  
 ; REFERENCE/DOCKET NUMBER: A2582-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (610)454-3839  
 ; TELEFAX: (610)454-3808  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1382 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 312..1370  
 ; US-08-985-492-3  
 Query Match 5.3%; Score 74.6; DB 4; Length 1382;  
 Best Local Similarity 53.9%; Pred. No. 4.7e-13;  
 Matches 202; Conservative 0; Mismatches 164; Indels 9; Gaps 2;  
 Qy 388 TACATCCATGCTGTAACAAATCTCCGTTGTTGGTCTGAGGTGCTTATTTATTTGAT 447  
 Db 702 TACACGGATCGGTCATATATACAGGGTGTGGACACAGCAATGCCAGGATGCTCGAC 761  
 Qy 448 GTTCTCATGAAAAAATTGAATATTCCTCTTAAAGTGCACTTGATTTGCCACAGCTTG 507  
 Db 762 TGGCTGCAGGAGAGGACGATTTTCTCTCGGAATGTCACATGATCGGCTACAGCCTC 821  
 Qy 508 GGAGCACACCTGGCTGGGAGCTGG--GTCAGGATACCGGCTTGGAGAGTAATCT 564  
 Db 822 GGAGCGCACGTGGCGGGTATGAGGCGGCGGACATCCGTAAGGAACGCTGGCGGATCACA 881  
 Qy 565 GGGTTGACCCAGCTGGGCGCATTTTCCACACACTCCAAAGGAAGTCAGGCTAGACCCC 624  
 Db 882 GGTTTGGATCTCGCGGCGCCATGTTTGAAGGGCGGCGACATCCACAGAGGCTCTCTCG 941  
 Qy 625 TCGGATGCCAATTTTGTGAGCTTATTCATAAATGCAAGTCCGATCTCTTTGAGCTT 684  
 Db 942 GACGATGCAGATTTTGTGAGTGTCTCCACACCTACACCGGTTCTCTCGGCTTGAGCAT 1001



## GENERAL INFORMATION:

APPLICANT: King, Te-Piao  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED  
THEREON  
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED  
THEREON  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/180,209B  
FILING DATE: 11-JAN-1994

## CLASSIFICATION:

CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/031,400

## ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-074 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

## INFORMATION FOR SEQ ID NO: 26:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1341 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 153..1052

8-180-209B-26

Query Match 3.1%; Score 43.4; DB 1; Length 1341;  
Best Local Similarity 50.9%; Pred. No. 0.0025;  
Matches 141; Conservative 0; Mismatches 121; Indels 15; Gaps 1;

396 TGCTGTAACAACTCCGGTGTGTTGGTGTGCTGAGGTGGCTTATTTTATTGATGTTCTCAT 455  
455 TGCTGCTAGAAATACACGTTTAGTTGGACAATATATCGTACGATTAACCCAGNAACTCGT 514  
456 GAAAAAATTTGAATATTCCTTCTAAAGTGCACCTTGAATGGCCACAGCTTGGAGGCACA 515  
515 AAAACACTATAAAATFCGATGGCAAAATATACGATTAATGGACATAGCTTAGGAGCACA 574  
516 CCTGGCTGGGAAGCTGGGTCAAGGATACAGGCTTGGAG-----AAT 560  
575 TGCCTCAGTTTTGCAGGCAAAAGGTTCAAGAGTTAAATTAGGAAATATTCGAAT 634  
561 AACTGGTGGTGAACCCAGCTGGGCCATTTTTCCCAACACTCCAAAGGAAGTCAGGCTAGA 620  
635 TATTGGGCTTGATCCTGCTAGGCCCTCGTTCGATTCAAATCATTTGCCGAAGACTCTG 694  
621 CCCCTCGATGCCAACTTTGTTGACGTTATTCATACA 657  
695 CGAGACAGATGCAGAAATATGTTCAAATATATACATACA 731

LT 9

3-385-745-26

; Sequence 26, Application US/08385745

; Patent No. 5612209

; GENERAL INFORMATION:

; APPLICANT: King, Te Piao

; TITLE OF INVENTION: Cloning and Recombinant Production of

; TITLE OF INVENTION: Vespil Venom Phospholipases, and Immunological Therapies

; TITLE OF INVENTION: Based Thereon

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/385,745

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/031,400

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 3288-020

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 790-9090

; TELEFAX: 212 869-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1341 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 153..1052

; US-08-385-745-26

Query Match 3.1%; Score 43.4; DB 1; Length 1341;  
Best Local Similarity 50.9%; Pred. No. 0.0025;  
Matches 141; Conservative 0; Mismatches 121; Indels 15; Gaps 1;

Qy 396 TGCTGTAACAACTCCGGTGTGTTGGTGTGCTGAGGTGGCTTATTTTATTGATGTTCTCAT 455  
Db 455 TGCTGCTAGAAATACACGTTTAGTTGGACAATATATCGTACGATTAACCCAGAACTCGT 514  
Qy 456 GAAAAAATTTGAATATTCCTTCTAAAGTGCACCTTGAATGGCCACAGCTTGGAGGCACA 515  
Db 515 AAAACACTATAAAATCTCGATGGCAAAATATACGATTAATGGACATAGCTTAGGAGCACA 574  
Qy 516 CCTGGCTGGGAAGCTGGGTCAAGGATACAGGCTTGGAG-----AAT 560  
Db 575 TGCCTCAGTTTTGCAGGCAAAAGGTTCAAGAGTTAAATTAGGAAATATTTCTGAAT 634  
Qy 561 AACTGGTGGACCCAGCTGGGCCATTTTTCCCAACACTCCAAAGGAAGTCAGGCTAGA 620  
Db 635 TATTGGGCTTGATCCTGCTAGGCCCTCGTTCGATTCAAATCATTTGCCGAAGACTCTG 694  
Qy 621 CCCCTCGATGCCAACTTTGTTGACGTTATTCATACA 657  
Db 695 CGAGACAGATGCAGAAATATGTTCAAATATATACATACA 731

RESULT 10

-485-388-26

ence 26, Application US/08485388

ent No. 6270763

NERAL INFORMATION:

APPLICANT: King, Te Piao

TITLE OF INVENTION: Cloning and Recombinant Production of

TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies

TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,388

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/385,745

FILING DATE: 08-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/031,400

FILING DATE: 11-MAR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-074 FMCA

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

FORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 1341 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 153..1052

-485-388-26

ty Match 3.1%; Score 43.4; DB 3; Length 1341;

t Local Similarity 50.9%; Pred. No. 0.0025;

ches 141; Conservative 0; Mismatches 121; Indels 15; Gaps 1;

396 TCGTGTAAACAATCTCCGTTGTGTGCTGAGTGGCTTATTTTATTGATGTTCTCAT 455

455 TCGTGTAGAAATACACGTTTAGTTGGCAATATATCGTACGATTACCCAGAACTCGT 514

456 GAAAAAATTTGAATATCCCTTCTTAAAGTGCACCTTGAATGGCCACAGCTTGGGAGCACA 515

515 AAAACACATATAAAATCTCGATGGCAAAATATACGATTAATTGGACATAGCTTAGGAGCACA 574

516 CTGGCTGGGGAAGCTGGGTCAAGGATACCAAGGCTTGGGAAG-----AAT 560

575 TGCTTCAGGTTTTCAGGCAAAAAGGTTCAAGAGTTAAATAGGAAATATCTGAAAT 634

561 AACTGGTTGGACCCAGCTGGGCCATTTTCCACAACACTCCAAAGGAAGTCAAGGCTAGA 620

635 TATTGGGCTTGATCCTGCTAGGCCCTTCGTTGGTTCGATCAATCAATGTTCCGAAAGACTCTG 694

QY 621 CCCTCGGATGCCAACTTTTGTGTGACGTTATTCATACA 657

Db 695 CGAGACAGATGCAGATATGTTCAAATATACATACA 731

RESULT 11

US-08-474-853-26

; Sequence 26, Application US/08474853

; Patent No. 6287559

; GENERAL INFORMATION:

; APPLICANT: King, Te-Piao

; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND

; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON

; NUMBER OF SEQUENCES: 62

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/474,853

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/180,209

; FILING DATE: 11-JAN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/031,400

; FILING DATE: 11-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-074 CIPB

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1341 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 153..1052

US-08-474-853-26

Query Match 3.1%; Score 43.4; DB 3; Length 1341;

Best Local Similarity 50.9%; Pred. No. 0.0025;

Matches 141; Conservative 0; Mismatches 121; Indels 15; Gaps 1;

QY 396 TCGTGTAAACAATCTCCGTTGTGTGCTGAGTGGCTTATTTTATTGATGTTCTCAT 455

Db 455 TCGTGTAGAAATACACGTTTAGTTGGCAATATATCGCTACGATTACCCAGAACTCGT 514

QY 456 GAAAAAATTTGAATATCCCTTCTTAAAGTGCACCTTGAATGGCCACAGCTTGGGAGCACA 515

Db 515 AAAACACATATAAAATCTCGATGGCAAAATATACGATTAATTGGACATAGCTTAGGAGCACA 574

QY 516 CTGGCTGGGGAAGCTGGGTCAAGGATACCAAGGCTTGGGAAG-----AAT 560

Db 575 TGCTTCAGGTTTTCAGGCAAAAAGGTTCAAGAGTTAAATAGGAAATATCTGAAAT 634

561 AACTGGGTGGACCCAGCTGGCGCATTTTCCACACACTCCAAAGAGTCAAGGCTAGA 620  
562 TTTTGGGCTTGTATCTGCTAGGCTTGGTTCAATCAATTTCCGAAAGACTCTG 694  
621 CCCCTCGATGCCAAGCTTTGTTGACGTTATTCATACA 657  
695 CGAGACAGATGCAGATATGTTCAAAATTATACATACA 731

LT 12  
9-166-205B-26  
Sequence 26, Application US/09166205B  
Ent No. 6372471  
GENERAL INFORMATION:  
APPLICANT: Te Piao KING  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,  
TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL  
TITLE OF INVENTION: THERAPIES BASED THEREON  
FILE REFERENCE: 2313/OF138US  
CURRENT APPLICATION NUMBER: US/09166.205B  
CURRENT FILING DATE: 1998-10-01  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: FastSeq for Windows Version 3.0  
Q ID NO 26  
LENGTH: 1341  
TYPE: DNA  
ORGANISM: Vespula vulgaris  
9-166-205B-26

Query Match 3.1%; Score 43.4; DB 4; Length 1341;  
Best Local Similarity 50.9%; Pred. No. 0.0025;  
Matches 141; Conservative 0; Mismatches 121; Indels 15; Gaps 1;  
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455 TGCTGTAGAATAACAGTTAGTTGGCAATATATCGTACGATTACCCAGAACTCGT 514  
456 GAAAAAATTTGAATATTTCCCTTCTAAAGTGCACCTGATGGCCACAGCTTGGGAGCACA 515  
515 AAAACACTATAAATCTCGATGGCAATATACGATTAAATTTGGACATAGCTTAGGAGCACA 574  
516 CCTGGCTGGGAACTGGTTCAGGATACAGGCTTGGAG-----AAT 560  
575 TGCTTCAGTTTTCGAGGCAAAAGGTTCAAGAGTTAAATTTAGGAAAAATATTTCTGAAT 634  
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635 TATTGGGCTTGTATCTGCTAGGCTTGGTTCAATCAATCATTTTCCGAAAGACTCTG 694  
621 CCCCTCGATGCCAAGCTTTGTTGACGTTATTCATACA 657  
695 CGAGACAGATGCAGATATGTTCAAAATTATACATACA 731

LT 13  
US94-02629-26  
Sequence 26, Application PC/TUS9402629  
GENERAL INFORMATION:  
APPLICANT: King, Te-Piao  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02629  
FILING DATE: 10-MAR-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/180,209  
FILING DATE: 11-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/031,400  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-074 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1341 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 153..1052  
PCT-US94-02629-26

Query Match 3.1%; Score 43.4; DB 5; Length 1341;  
Best Local Similarity 50.9%; Pred. No. 0.0025;  
Matches 141; Conservative 0; Mismatches 121; Indels 15; Gaps 1;  
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Db 695 CGAGACAGATGCAGATATGTTCAAAATTATACATACA 731

RESULT 14  
US-08-446-855A-1/c  
Sequence 1, Application US/08446855A  
Patent No. 5845573  
GENERAL INFORMATION:  
APPLICANT: Stewart, Thomas S  
APPLICANT: Flores, Maria V  
APPLICANT: O'Sullivan, William J  
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl  
TITLE OF INVENTION: phosphate synthetase II  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 1100 No. 5649573th Glebe Road, 8th Floor  
CITY: Arlington  
STATE: Virginia



COUNTRY: USA  
 ZIP: 22201-4714  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.24  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,855A  
 FILING DATE: 06-Jul-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mitchard, Leonard C  
 REGISTRATION NUMBER: 29,009  
 REFERENCE/DOCKET NUMBER: 47-80  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-816-4000  
 TELEFAX: 703-816-4100  
 FORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8920 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: genomic  
 -446-855A-1

Query Match 2.8%; Score 39.2; DB 2; Length 8920;  
 Best Local Similarity 46.4%; Pred. No. 0.15;  
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 QY 823 TTGACTGTAAACCATGCCCGAAGTTATCAATTTTATGCTGAAAGCATTTCTTAATCCTGAT 882  
 Db 8798 AATTATTATATAATTAAGAAGATTTATACATTTTAAATGTTTATATATTTTATTTT 8739  
 QY 883 GCATTTATGCTTATCCTTTGTAGATCCACACATCTTTTAAAGCAGGAATGCTTCTTT 942  
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 Db 8678 TTATACATATGATGAATAATAAATTTGTATATATACAAAATTTTAAAAAATAA 8619  
 QY 1003 ATGAAGACTAATGGATCACAATTATTTTAAACACA 1038  
 Db 8618 ATCAATATAAATTAATGATCATATTTTAAATAAAAAACA 8583

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 Job time : 102 secs

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 ent No. 6183996  
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 PLICANT: Stewart et al.  
 FILE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate  
 ent No. 6183996  
 FILE OF INVENTION: Synthetase II  
 LE REFERENCE:  
 XRENT APPLICATION NUMBER: US/09/150,741  
 XRENT FILING DATE: 1998-09-10  
 XLIER APPLICATION NUMBER: PL6380  
 XLIER FILING DATE: 1992-12-16  
 XLIER APPLICATION NUMBER: AU93/00617  
 XLIER FILING DATE: 1993-12-02  
 XLIER APPLICATION NUMBER: 08/446,855  
 XLIER FILING DATE: 1995-07-06  
 XLIER OF SEQ ID NOS: 15  
 TWARE: PatentIn Ver. 2.0  
 ID NO 1

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um DB seq length: 0

um DB seq length: 2000000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

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17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2527	100.0	467	9	US-09-735-933-2	Sequence 2, Appli
2527	100.0	467	14	US-10-038-517-2	Sequence 2, Appli
2523	99.8	467	12	US-10-403-745-3	Sequence 3, Appli
2276	90.1	461	12	US-10-312-088-23	Sequence 23, Appli
1191	47.1	469	9	US-09-735-933-4	Sequence 4, Appli
1180	46.7	467	9	US-09-735-933-5	Sequence 5, Appli
1180	46.7	473	12	US-10-403-745-7	Sequence 7, Appli
1174	46.5	467	12	US-10-403-745-9	Sequence 9, Appli
1172	46.4	467	9	US-09-735-933-6	Sequence 6, Appli
1172	46.4	473	12	US-10-403-745-8	Sequence 8, Appli
1166	46.1	467	12	US-10-403-745-10	Sequence 10, Appli
1162	46.0	467	12	US-10-403-745-4	Sequence 4, Appli
1152	45.6	469	12	US-10-403-745-5	Sequence 5, Appli
1152	45.6	477	9	US-09-925-297-739	Sequence 739, App
1115	44.1	465	9	US-09-923-779-151	Sequence 151, App

16	1115	44.1	465	12	US-10-403-745-6	Sequence 6, Appli
17	1115	44.1	473	15	US-10-128-449A-15	Sequence 15, Appli
18	1115	44.1	465	9	US-09-925-297-567	Sequence 567, App
19	576	22.8	329	15	US-10-163-547-5	Sequence 5, Appli
20	534	21.1	499	11	US-09-802-640-20	Sequence 20, Appli
21	534	21.1	499	15	US-10-128-449A-14	Sequence 14, Appli
22	515.5	20.4	452	12	US-10-312-088-37	Sequence 37, Appli
23	515.5	20.4	500	12	US-10-354-358-46	Sequence 46, Appli
24	515.5	20.4	500	15	US-10-128-449A-8	Sequence 8, Appli
25	513	20.3	451	15	US-10-163-547-3	Sequence 3, Appli
26	513	20.3	451	15	US-10-157-031-76	Sequence 76, Appli
27	513	20.3	451	15	US-10-220-380-5	Sequence 5, Appli
28	462.5	18.3	345	15	US-10-128-449A-10	Sequence 10, Appli
29	462.5	18.3	353	15	US-10-128-449A-4	Sequence 4, Appli
30	462.5	18.3	354	10	US-09-978-295A-178	Sequence 178, App
31	462.5	18.3	354	10	US-09-978-697-178	Sequence 178, App
32	462.5	18.3	354	10	US-09-978-192A-178	Sequence 178, App
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34	462.5	18.3	354	11	US-09-978-189-178	Sequence 178, App
35	462.5	18.3	354	11	US-09-978-608A-178	Sequence 178, App
36	462.5	18.3	354	11	US-09-978-585A-178	Sequence 178, App
37	462.5	18.3	354	11	US-09-978-191A-178	Sequence 178, App
38	462.5	18.3	354	11	US-09-978-403A-178	Sequence 178, App
39	462.5	18.3	354	11	US-09-978-564A-178	Sequence 178, App
40	462.5	18.3	354	11	US-09-999-833A-178	Sequence 178, App
41	462.5	18.3	354	11	US-09-981-915A-178	Sequence 178, App
42	462.5	18.3	354	11	US-09-978-824-178	Sequence 178, App
43	462.5	18.3	354	11	US-09-978-585A-178	Sequence 178, App
44	462.5	18.3	354	11	US-09-978-423A-178	Sequence 178, App
45	462.5	18.3	354	11	US-09-978-193A-178	Sequence 178, App

ALIGNMENTS

RESULT 1  
US-09-735-933-2  
; Sequence 2, Application US/09735933  
; Patent No. US20020052034A1  
; GENERAL INFORMATION:  
; APPLICANT: GUEGLER, Karl et al  
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO00863  
; CURRENT APPLICATION NUMBER: US-09-735-933-  
; CURRENT FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Human  
US-09-735-933-2

Query Match 100.0%; Score 2527; DB 9; Length 467;  
Best Local Similarity 100.0%; Pred. No. 9.2e-245;  
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 CRSYTSFKAGNCFKSCGECPTMGHPADRFHFNKMTNGSHYFLNTGSLSPFARWRHKL 360  
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361 VKLSGSEVTQGTFLRVGGAGKGTGEPAIVSGKLEPGMTYTKLIDADVNGNITSVQFIW 420  
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J T 2  
J-038-517-2  
Sequence 2, Application US/10038517  
Publication No. US20020115844A1  
GENERAL INFORMATION:  
APPLICANT: Yu, Xuanchuan  
PPLICANT: Turner, C. Alexander Jr.  
TITLE OF INVENTION: No. US20020115844A1 Human Lipase and Polynucleotides Encoding b  
FILE REFERENCE: LEX-0293-USA  
CURRENT APPLICATION NUMBER: US/10/038, 517  
CURRENT FILING DATE: 2002-01-03  
PRIOR APPLICATION NUMBER: US 60/259, 830  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 4.0  
2 ID NO 2  
LENGTH: 467  
TYPE: PRT  
ORGANISM: homo sapiens  
J-038-517-2  
Query Match 100.0%; Score 2527; DB 14; Length 467;  
Best Local Similarity 100.0%; Pred. No. 9.2e-245;  
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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421 KXHLFEDSQNKLGAEMVINTSGKYGKSTFCSDIMGNILQNLKPC 467  
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181 IPGLGRITGLDPAGPFPHNTPKFVRLDPSDANFVDVHTNAARILFELGVGTIDACGHL 240  
421 KXHLFEDSQNKLGAEMVINTSGKYGKSTFCSDIMGNILQNLKPC 467  
RESULT 3  
US-10-403-745-3  
Sequence 3, Application US/10403745  
Publication No. US20030165975A1  
GENERAL INFORMATION:  
APPLICANT: Khodadoust, Mehran  
APPLICANT: Kapeller-Libermann, Rosana  
TITLE OF INVENTION: No. US20030165975A1 Human Lipase Proteins, Nucleic Acides Encod  
FILE REFERENCE: 10147-14  
CURRENT APPLICATION NUMBER: US/10/403, 745  
CURRENT FILING DATE: 2003-03-31  
PRIOR APPLICATION NUMBER: US/09/411, 132A  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-403-745-3  
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Best Local Similarity 99.8%; Pred. No. 2.3e-244;  
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Db 121 LDWINGSREYTHAVNNLRVVGAEVAFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180  
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Db 181 IPGLGRITGLDPAGPFPHNTPKFVRLDPSDANFVDVHTNAARILFELGVGTIDACGHL 240  
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Db 241 FYPNGGKHPGCCDLITPLLKFNFNAYKKEMASFFDCNARSYQFYAESILNPDFAIAYP 300  
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Sequence 23, Application US/10312088  
Publication No. US20030219862A1  
GENERAL INFORMATION:  
APPLICANT: Agarwal, Pankaj  
APPLICANT: Cogswell, John P.  
APPLICANT: Kabanic, Karen S.  
APPLICANT: Lai, Ying-Ta  
APPLICANT: Martensen, Shelby A.

```

P1ICANT: Murdock, Paul R.
P1ICANT: Smith, Randall F.
P1ICANT: Strum, Jay C.
P1ICANT: Xiang, Zhaoxing
P1ICANT: Xie, Qing
P1ICANT: Rizni, Safia K.
FILE OF INVENTION: NOVEL COMPOUNDS
LE REFERENCE: GF50029
RRNT APPLICATION NUMBER: US/10/312,088
RRNT FILING DATE: 2002-12-20
IOR APPLICATION NUMBER: PCT/US01/19929
IOR FILING DATE: 2001-06-22
IOR APPLICATION NUMBER: 60/213,161
IOR FILING DATE: 2000-06-22
IOR APPLICATION NUMBER: 60/213,156
IOR FILING DATE: 2000-06-22
MBER OF SEQ ID NOS: 44
FTWARE: FastSeq for Windows Version 4.0
ID NO 23
ENGTH: 461
YPE: PRT
GANISM: Homo sapiens
-312-088-23

ry Match          90.1%; Score 2276; DB 12; Length 461;
t Local Similarity 91.5%; Pred. No. 1.4e-219;
ches 431; Conservative 8; Mismatches 18; Indels 14; Gaps 3

1  MLCGIWIVAEFLFTGTRGRKEVCYERLGCFCGDLPTWRTFTSTELVGLPWSPEKINTRFLLYT 60
1  MLCGIWIVAEFLFTGTRGRKEVCYERLGCFCGDLPTWRTFTSTELVGLPWSPEKINTRFLLYT 60

61  IHNPNAYQIISAVNSSTIQASVFGTDKITRINIAGWKTDCKWORDMCNVLLQEDINCIN 120
61  IHNPNAYQIISAVNSSTIQASVFGTDKITRINIAGWKTDCKWORDMCNVLLQEDINCIN 120

121  LDWINGSREYIHAVNNLRVGAEVAYFDIVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180
121  LDWINGSREYIHAVNNLRVGAEVAYFDIVLMKKFEYSPSKVHLIGHSLGAHLAGEAGSR 180

181  IPCGLRITGLDPAAGPFFHTPREVLDPDSDFVVDVHTNAAAILFELGVGTIDACGHL 240
181  IPCGLRITGLDPAAGPFFHTPREVLDPDSDFVVDVHTNAAAILFELGVGTIDACGHL 240

241  FYPNGGKHPGCCEDLITPLLKFNFNAYKENAFDNCNHARSQFYAESILNPDAFIAP 300
241  FYPNGGKHPGCCEDLITPLLKFNFNAYKENAFDNCNHARSQFYAESILNPDAFIAP 300

301  CRSYTSFKAGNCFPCSKGCGPTMGHFADRPFFKNMKNTHGSHYFLNTG----SLSPFARWR 356
301  CRSYTSFKAGTCV----GCADLLHRIDK-----IGSHTSHVFLTSLPFLVLSYLGWR 350

357  HKLSVKLSGSSEVTQGTVFLRVGGAIGKTGEFAIVSGKLEPGMYTKLIDADVNVGNITSV 416
351  HKLSVKLSGSSEVTQGTVFLRVGGAIVKTGEFAIVSGKLEPGMYTKLIDADVNVGNITSV 410

417  QFTWKHKLPEDSQNLGAEMVINTSGKYGYKSTFCSDQIMGNILQNLKPC 467
411  QFTWKHKLPEDSQNLGAEMVINTSGKYGYKSTFCSDQIMGNILQNLKPC 461

F 5
-735-933-4
rence 4, Application US/09735933
ent No. US2002052034A1
ERAL INFORMATION:
P1ICANT: GUEGLER, Karl et al
FILE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USSE
LE REFERENCE: CLO00863
FILE OF INVENTION: THEREOF
RRNT APPLICATION NUMBER: US/09/735,933
RRNT FILING DATE: 2000-12-14

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Myocastor_coryus
US-09-735-933-4

Query Match      47.1%; Score 1191; DB 9; Length 469;
Best Local Similarity 49.8%; Pred. No. 1.3e-110;
Matches 236; Conservative 63; Mismatches 163; Indels 12; Gaps 7;

QY  1  MLGIWIVARLFPGTSRGKVCYERLGCFCXGDLGDPWTRTFSTELVGLDPSKPKINTRLFLYY 60
DB  1  MLFWITGCLLLLTARGNEVCYSHLGCFCDEKFWAGTLORPVKSLSFASDESINTRFLYY 60

QY  61  IHNPNAYQEISAVNSSTIOASYFGTDKTRINAGWKTDGK--WQDMCNVLLQLQLEDINC 118
DB  61  NENPNYQLITATDPATIKASNFNLHKKTRFVIHGFIENGEDWLTDICKRMFQVEKVC 120

QY  119  INLDWINGSRE-VIHAVNLRVVGAVAYFIDVLMKKFPYSPKVLHGSLGAHLAGEA 177
DB  121  ICVDWGGSLAIYSQAVQIRVVGAVALVQLSDQLGYKPGNVMHIGHSLGAHTAAEA 180

QY  178  GSRIPGL-GRITGLDPAGPFPHNTPKVERLDPSDANFVDVHTNNAARILFELCGVGTIDAC 236
DB  181  GRRLKGLVGRITGLDPAECFQDTPFEVLDPDSANFVDVHTDIAPIPSFGFGMSQKV 240

QY  237  GHLDYFVNGKHPGGE-DLIITLLKFNPNAYKEMASPFDCNHAASYQFYAESILNPDA 295
DB  241  GHMDFPFGKEMPGCEKNIISTIV--DVNGFLEGITSLAACNHNMSYQYVSSSILNPDG 298

QY  296  FIAYPCRSYTSFKAGNCFECSKEGCPCTMGHADRHFKNMKTNG--SHYFLNTGSLSPFA 353
DB  299  FLGYPCASVEEFGKCGFCPCPAGCCPMGHYADQF---QKGANGVEKTYFLNTGSDSNPP 355

QY  354  RWSHKLSVKLSGSEVYQGTVFLRVGGAIGKTGEFAIVSGKLBPGMTYTKLIADVNVGNI 413
DB  356  RWYKYSVTLSGEKLSGDIKIALFGRNGNSKQYEIYFKGLSPXDARYTHDIDVDLVNGEI 415

QY  414  TSVQFTWKXHLFEDSQNKLAGAEVINTSKYGYKSTFCQDIMGPNILQNLKPC 467
DB  416  QKYKFLMHNNGINLLQPKLQSQITVQSGEYGTKNFCCSNTVQEDVLQSLSPC 469

RESULT 6
US-09-735-933-5
; Sequence 5, Application US/09735933
; Patent No. US20020052034A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000863
; CURRENT APPLICATION NUMBER: US/09/735,933
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus_musculus
US-09-735-933-5

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Query Match      46.7%; Score 1180; DB 9; Length 467;
Best Local Similarity 49.0%; Pred. No. 1.7e-109;
Matches 231; Conservative 73; Mismatches 159; Indels 8; Gaps 6;

Qy  1  MLCGIMIVAPLFGTSGKVEVCYERLCGFCFDDGHPWTRTSTELVGLPWPSEKINTREFLYT  60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  1  MLILMTIPFLFLGAAGKVEVCYDNLGCSDFAPWAGTARPKLFLPWPSEKINTREFLYT  60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

51

-735-933-4  
rence 4, Application US/09735933  
pat No. US20020052034A1  
ERAL INFORMATION:  
PLICANT: GUEGLER, Karl et al  
TILE OF INVENTION: ISOLATED HUMAN LIPIASE PROTEINS, NUCLEIC  
FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPIASE PROTEINS, AND USSES  
FILE OF INVENTION: THEREOF  
LE REFERENCE: CL000863  
RENT APPLICATION NUMBER: US/09/735,933  
RENT FILING DATE: 2000-12-14



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T 9
-735-933-6
nence 6, Application US/09735933
ent No. US20030165975A1
ERAL INFORMATION:
PLICANT: GUEGLER, Karl et al
LE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
LE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
LE OF INVENTION: THEREOF
LE REFERENCE: CLO00863
RENT APPLICATION NUMBER: US/09/735,933
RENT FILING DATE: 2000-12-14
MBER OF SEQ ID NOS: 6
WARE: FastSeq for Windows Version 4.0
ID NO 6
ENGTH: 467
YPE: PRT
RGANISM: Rattus_norvegicus
-735-933-6

ry Match 46.4%; Score 1172; DB 9; Length 467;
t Local Similarity 49.3%; Pred. No. 1.1e-108;
ches 232; Conservative 73; Mismatches 158; Indels 8; Gaps 6;

1 MLGIWIVAFLEFCTSRGKEVCYERLGCCKDGLPWTFTSTELVGLPWSPEKINTREFLLYT 60
1 MLTLWTVSLFLGAAQGEVCYDNLGCFSDAEPWAGTAIRPLKLLPWSPEKINTREFLLYT 60
61 IHNPNAYQIEISAVNSSTIOASYFGTDKITRINIAGW--KTDGKWQORDMNCVLLQLEDINC 118
61 NENPTAFQTLQSLDPLTIGASNFQVARKTRFIHGFIDKGEENWVDMCKMNFQVEVNC 120
119 INLDWINGSR-EYIHAVNNLRVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177
121 ICVDWKKGSQTTYTOAANNVRVGAQVAMIDILVKNSYSYSPSKVHLIGHSLGAHVAGEA 180
178 GSRIPGLGRITGLDPAGPFPHNTPKVEVLDPDSANFVDVHTNAARILFELGVGTIDACG 237
181 GSRTPLGLRITGLDPVEANFEGTPEEVLDPDSADFVDVHTDAAPLIPFLPGFTNOMSG 240
238 HLDYFNGGKHPGC-EDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESILNPDFA 296
241 HLDFFNGGQMPGCKKNALSQIV--DIDGIWSGTRDFVACNHLRSYKYLESILNPDGF 298
297 IAYPCRSYTSFKAGNCFCKGCGPTMGHFADRPHFKMKTNGSHYFLNTGSLSPFARWR 356
299 AAYPCASYKDFESNCKFCPCDQCGPQMGHYADKFAGKS-GDEPKQFFLNTGEAKNFARWR 357
357 HKLSVKLSGSEVTQGTVFLRVGGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416
358 YRVSLILSGRMT-GQVKVALFGSKGNTRQYDIFRGIKPGATHSSSEFADKLDVGTIEKV 416
417 QFTWKXHLFEDSQNKLGAEWVINTSGKYKSTFCSDQIMGNILQNKPC 467
417 KFLWNNQVINPSPKVGAAKITVQKGEERTYFNFCSEETVREDTLLTLLEC 467

T 10
-403-745-8
nence 8, Application US/10403745
lication No. US20030165975A1
ERAL INFORMATION:
PLICANT: Khodadoust, Mehran
PLICANT: Kapeller-Libermann, Rosana
LE OF INVENTION: No. US20030165975A1el Human Lipase Proteins, Nucleic Acides Encod
LE OF INVENTION: Them, and Uses of Both of These
LE REFERENCE: 10147-14
RENT APPLICATION NUMBER: US/10/403,745
RENT FILING DATE: 2003-03-31
IOR FILING DATE: 2000-09-12
MBER OF SEQ ID NOS: 10

```

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-403-745-8

Query Match 46.4%; Score 1172; DB 12; Length 473;
Best Local Similarity 49.3%; Pred. No. 1.1e-108;
Matches 232; Conservative 73; Mismatches 158; Indels 8; Gaps 6;

QY 1 MLGIWIVAFLEFCTSRGKEVCYERLGCCKDGLPWTFTSTELVGLPWSPEKINTREFLLYT 60
DB 1 MLTLWTVSLFLGAAQGEVCYDNLGCFSDAEPWAGTAIRPLKLLPWSPEKINTREFLLYT 60
QY 61 IHNPNAYQIEISAVNSSTIOASYFGTDKITRINIAGW--KTDGKWQORDMNCVLLQLEDINC 118
DB 61 NENPTAFQTLQSLDPLTIGASNFQVARKTRFIHGFIDKGEENWVDMCKMNFQVEVNC 120
QY 119 INLDWINGSR-EYIHAVNNLRVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177
DB 121 ICVDWKKGSQTTYTOAANNVRVGAQVAMIDILVKNSYSYSPSKVHLIGHSLGAHVAGEA 180
QY 178 GSRIPGLGRITGLDPAGPFPHNTPKVEVLDPDSANFVDVHTNAARILFELGVGTIDACG 237
DB 181 GSRTPLGLRITGLDPVEANFEGTPEEVLDPDSADFVDVHTDAAPLIPFLPGFTNOMSG 240
QY 238 HLDYFNGGKHPGC-EDLITPLKFNFNAYKEMASFFDCNHARSYQFYAESILNPDFA 296
DB 241 HLDFFNGGQMPGCKKNALSQIV--DIDGIWSGTRDFVACNHLRSYKYLESILNPDGF 298
QY 297 IAYPCRSYTSFKAGNCFCKGCGPTMGHFADRPHFKMKTNGSHYFLNTGSLSPFARWR 356
DB 299 AAYPCASYKDFESNCKFCPCDQCGPQMGHYADKFAGKS-GDEPKQFFLNTGEAKNFARWR 357
QY 357 HKLSVKLSGSEVTQGTVFLRVGGAIGKTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416
DB 358 YRVSLILSGRMT-GQVKVALFGSKGNTRQYDIFRGIKPGATHSSSEFADKLDVGTIEKV 416
QY 417 QFTWKXHLFEDSQNKLGAEWVINTSGKYKSTFCSDQIMGNILQNKPC 467
DB 417 KFLWNNQVINPSPKVGAAKITVQKGEERTYFNFCSEETVREDTLLTLLEC 467

RESULT 11
US-10-403-745-10
; Sequence 10, Application US/10403745
; Publication No. US20030165975A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: No. US20030165975A1el Human Lipase Proteins, Nucleic Acides Encodi
; TITLE OF INVENTION: Them, and Uses of Both of These
; FILE REFERENCE: 10147-14
; CURRENT APPLICATION NUMBER: US/10/403,745
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US/09/411,132A
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-403-745-10

Query Match 46.1%; Score 1166; DB 12; Length 467;
Best Local Similarity 48.0%; Pred. No. 4.3e-108;
Matches 226; Conservative 79; Mismatches 158; Indels 8; Gaps 6;

QY 1 MLGIWIVAFLEFCTSRGKEVCYERLGCCKDGLPWTFTSTELVGLPWSPEKINTREFLLYT 60
DB 1 MVSINTIALFLLGAQKAEVCYEQIGCFSDAEPWAGTAIRPLKVLPLWSPEKINTREFLLYT 60

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61 IHNNAYQEI SAVNSS TIOASYGCTDKAITINAGW--KTDGKQDQDMCNVLLOLEDINC 118
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
61 NKNFNNTQTLLPDSPTIEASNFO TDKKTFTI LHGFTDKGEENWLLDMCKNMPKVEAVNC 120
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
119 INLDWINGSR-EYIHA VNNLRVVGAEVAYEIDVLMKFEYSPSKVLHGHS LGHAHAGEA 177
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
121 ICVDWKGSQTSY TQAANNVRVVGAAQVAML SMLSANYSPSQVQLI GHSLGAHVAGEA 180
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
178 GSRIPGLGRITGLDPAGCFPHNTPKVR LDPDSANFVDVHTHNAAILPBLGVGTTDAG 237
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
181 GSRTPGUGRITGLDPV EAS TQGTPEEVR LDPDTADFDVDVHTHDAAPLIPFLGFGTSQQMG 240
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
238 HLDFFYPNGGKHMPCG-EDLITPLLKFNFNAYKKEMASFPDCHNARSGVQFYAESILNPDAF 296
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
241 HLDFFPNPNGEEMPCKKNALSQIV--DL DGIWEGTRDPVACNHLRSYKYSESILNPDOF 298
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
297 IAYPCRSYTFEFKAGNCFECSKEGCP TWHGFADRFHFKNMKTNGSHVFLNTGSLSPFARWR 356
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
299 ASYPCASYRAFESKNCEP CDPQCPQMGHYADFEAVKT-SDETQYFLNTGSSSNFARWR 357
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
357 HKLSVKLSGSSEV TQGTVFLRVGGAIGKTGEFAFVS GKLPEGMYTKLIDADVNVGNITSV 416
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
358 YGVSIITLSGKRAT-GQAKVALFGSKGNTHQFNIFKILP EGSHTSNEFPAKLDVGTIEKV 416
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
417 QFTWKXHLFPDSQNKLGAEVINTS GKYGYKSTFCQSODIMGPNILQNLKPC 467
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
417 KFLWNNVNVNPTPKVGA AKITVQKGEETKTVHSFCSESTVREDVLLTLTPC 467
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

LT 12  
0-403-745-4  
quence 4, Application US/10403745  
plication NO. US20030165975A1  
NERAL INFORMATION:  
PPPLICANT: Khodadoust, Mehran  
PPPLICANT: Kapeller-Libermann, Rosana  
TITLE OF INVENTION: NO. US20030165975A1 Human Lipase Proteins, Nucleic Ac  
ITLE OF INVENTION: them, and Uses of Both of These  
ILE REFERENCE: 10147-14  
URRENT APPLICATION NUMBER: US/10/403,745  
URRENT FILING DATE: 2003-03-31  
RIOR APPLICATION NUMBER: US/09/411,132A  
RIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 10  
FTWARE: PatentIn Ver. 2.1  
2 ID NO 4  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Homo sapiens  
0-403-745-4

[illegible]

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Db 241 HLDFFNGGESPGCKQNALQOIV--DDGIWAGTRDFVACNHLRSYKYYLESILNPDGG 256
QY 297 IAYPCRSYTSFAGNCGFFCSKEGCPTMGHFPADRFHFNKMKTNGSHYFLNTGSLSPFARWR 356
Db 299 AAYPCTSYKSFSDKCFPCDQCGCPQMGHYADKAGTSEQ_QKFPNTGEASNFARWR 357
QY 357 HKLSVKLSGSEVTQGTVFLRVGGAIGKTGEBFAIVSGKLEFGMYTKLIDADVNVGNITSV 416
Db 358 YGVSIITLSKRTAT-GOI KVALFGNKNTHQYSIFRGILKPGSTHSYEFDAKLVDVGTIKV 416
QY 417 QFTWKKHLPEDSQNLGAEMVINSGKYGYKSTFCSDQIMGPNILQNLKPC 467
Db 417 KELANNVINPLPKVGATKITVQKEGKTVYFCSSEDTVREDTLLTLTPC 467

RESULT 13
US-10-403-745-5
; Sequence 5, Application US/10403745
; Publication No. US20030165975A1
; GENERAL INFORMATION:
; APPLICANT: Kocadoust, Mehran
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: No. US20030165975A1el Human Lipase Proteins, Nucleic Ac
; TITLE OF INVENTION: Them, and Uses of Both of These
; FILE REFERENCE: 10147-14
; CURRENT APPLICATION NUMBER: US/10/403.745
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US/09/411,132A
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-745-5

```

Query Match	45.6%	Score 1152;	DB 12;	Length 469;
Best Local Similarity	47.8%;	Pred. No. 1.1e-106;		
Matches 225;	Conservative 68;	Mismatches 172;	Indels 6;	Gaps 5
Qy	1	MLGIWVAFPFSGTSGRKEVCYBERLGCFCGDKGLPWTWTFSTELVGLPWSPEKINTRFLVYT	60	
Db	1	MLPPPTIGILLLATVRGKEVCYQGCFCSDKEKWAGTLQRPVKLLPWSFEDIDTRFLVYT	60	
Qy	61	INNPNAYDEISAVNSSTIQSYFTGDKITRINIAGW--KTDGKWQBDMNCVLLQEDINC	118	
Db	61	NENPNNFOLITCTBPDTEASNFQLDKRTKTFIIHGFLDKAEDSWPSDMCKMFEVKYVC	120	
Qy	119	INLDWINGSRE-YTHAVNNLRVGAEVAVIDVLMKKFEYSPSKVHLGHSLGHAHGEA	177	
Db	121	ICVDRHRSRMYTQAVQNTIRVGAETAFIIQLSLTQLGYSLEDVHVIGHSLGANTAAEA	180	
Qy	178	GSRIPE-LGRITGLDPAGPFPHNTPEKVRLLDPDSANFVDVIHTNAARLFIELGVGTIDAC	236	
Db	181	GRRLGGRVGRITGLDPAGPCFQDBEPBEVRLLDPDAVFVDVIHTDSSPIVPSLGFQMSQKV	240	
Qy	237	GHLDFVYNGGKHEGECEDLITPLLKNFNAYKKEMASFFDCNHHASYSQYAEASILNPDAF	296	
Db	241	GHLDFPFGGKEMPCCKKNVLSIT-DIDIGEGIGFTVSCNHLRSFEYISSVNLNPGF	299	
Qy	297	IAYPCRSTSPKAGNCFFCSKEGCTPWGHFADRFHFKNMKTNGSHYFLNTGLSPFAWR	356	
Db	300	LGYPCASDYDFQESKCPCPAEGCPKMGHVADQKGTSAVEQT-FLFNTGSGNGFTSWR	358	
Qy	357	HKLIVKLSGSSEVGTGTVFLRVGGAIGTGEFAFVSQKLPBGWYTKLIDADVNVGNITSV	416	
Db	359	IKVSVTLGSKGVNGYIRIAYIGSNENSKQTEFKGSLRPDASHATCAIDVDFNVGKIQKV	418	
Qy	417	QPIWKHLFEDSQNLGAEMVINTSGKYGKSTFCSDQINGPNILQNLKPC	467	
Db	419	KFLMNKRGINLSEPKLGASOITVOSGDBGDEYFNFCSDTVBENVLOSILYPC	469	

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; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-779-151

Query Match      44.1%; Score 1115; DB 9; Length 465;
Best Local Similarity 47.8%; Pred No. 5,7e-103; Indels 14; Gaps 10;
Matches 226; Conservative 73; Mismatches 160;

QY 1 MGIWIVAFLEFSGTSRGEYERLGCDFKGLPWTTFSTELVGLPWSPEKINTRFLLYT 60
Db 1 MLPLWTLIS-LLLGAVAGKEVYERLGCDFSDSPWSGITTERPLHLPLWSPKDVNTRELLYT 59
QY 61 IHNPAYOEISAVNSSTIQASYFGTDKTRINIAGW--KTDGKQWQDMCNVLLQLEDINC 118
Db 60 NENPNFQEVAA--DSSSISGSNFKTNKTRFIHGFIDKGEENLANVCKNLFKVESVNC 118
QY 119 INLDWINGSRE-YIHAVNNLRVVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177
Db 119 ICVDWKGSGRTGYTCASQNIIVGAEVAYEVEFLQAGFYSPSNVHVIGHSLGAHLAGEA 178
QY 178 GSRIPG-LGRITGLDPAGPFHNTPEKVRLDPSDANFVDVHTNAARILFELGVGTIDAC 236
Db 179 GRRNTGTIGRITGLDPAEPCCFQGTPELVRLDPSDAKFVDVHTDGAPIVENLFGFMSQV 238
QY 237 GHLDFFPNGGKHMPCEDLITPLKFNFNAYKKEMASFFDCNHARSYQFYAESILNPDAF 296
Db 239 GHLDFFPNGGKHMPCCKNILSQI-VDIDGIEWGTRDFAACNHLRSYKYTDSIVNPDGF 297
QY 297 IAYPCRSTYTSFKAGNCFCSKEGCPMTGHPADRFHFNNKMTN--GSHYFLNTGSLSPFAR 354
Db 298 AGFPCASYNVFTANKCPSPGSGGCPQMGHYADRY---PGKTNDVGQKPYLDTGDASNPAR 354
QY 355 WRHKLVLKSGSEVTQGTFLRVGGAGIKGTGEFAIVSGKLEPGMTYTKLIDADVNGNIT 414
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QY 415 SVQFIWKXHLFEDSQNKLGAEVMVINTSGKYGKSTFCSDQIMGNILQNLKPC 467
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Search completed: January 6, 2004, 11:28:32
Job time : 53 secs
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I 14
-925-297-739
ence 739, Application US/09925297
nt No. US20020081659A1
RAL INFORMATION:
PLICANT: Rosen et al.
LE OF INVENTION: Nucleic Acids, Proteins and Antibodies
LE REFERENCE: PA105
RENT APPLICATION NUMBER: US/09/925,297
RRENT FILING DATE: 2001-08-10
OR APPLICATION NUMBER: PCT/US00/05989
OR FILING DATE: 2000-03-08
OR APPLICATION NUMBER: 60/124,270
OR FILING DATE: 1999-03-12
MBER OF SEQ ID NOS: 928
FTWARE: PatentIn Ver. 2.0
ID NO 739
NGTH: 477
YPE: PRT
GANISM: Homo sapiens
-925-297-739

ry Match      45.6%; Score 1152; DB 9; Length 477;
t Local Similarity 47.8%; Pred No. 1.1e-106; Indels 6; Gaps 5;
ches 225; Conservative 68; Mismatches 172;

1 MGIWIVAFLEFSGTSRGEYERLGCDFKGLPWTTFSTELVGLPWSPEKINTRFLLYT 60
9 MLPPWTGLILLATVRGECVCGQLGCFSDKPGWAGTLQRPVKLLPWSPEIDITRFLLYT 68
61 IHNPAYOEISAVNSSTIQASYFGTDKTRINIAGW--KTDGKQWQDMCNVLLQLEDINC 118
69 NENPNFQIITETPTIEASNFQLDKTRFIHGFIDKAEEDSPDMCKMEEVEKVCNC 128
119 INLDWINGSRE-YIHAVNNLRVVGAEVAYFIDVLMKKFEYSPSKVHLIGHSLGAHLAGEA 177
129 ICVDWHRGSRAMYTQAVQNIIVGAEVAYTAFLIQLSTQLGYSLDVEDVHVIGHSLGAHTAAEA 188
178 GSRIPG-LGRITGLDPAGPFHNTPEKVRLDPSDANFVDVHTNAARILFELGVGTIDAC 236
189 GRRLGRRVIRITGLDPAGPCFQDEPEEVRLDPSDAVFVDVHTDSSPIVPSLFGFMSQV 248
237 GHLDFFPNGGKHMPCEDLITPLKFNFNAYKKEMASFFDCNHARSYQFYAESILNPDAF 296
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297 IAYPCRSTYTSFKAGNCFCSKEGCPMTGHPADRFHFNNKMTN--GSHYFLNTGSLSPFARWR 356
308 LGYPCASYDEFQESKCFPCPAEGCPKMGHYADQFKGKTSAVEQT--PELNTGESGNFTSWR 366
357 HKLSVLKSGSEVTQGTFLRVGGAGIKGTGEFAIVSGKLEPGMTYTKLIDADVNGNITSV 416
367 YKVSUTLSGKKYNGYIIRLYGNSKQYEI FKGLKPDASHTCATDVIDVFNVGKIQKV 426
417 QFIWKXHLFEDSQNKLGAEVMVINTSGKYGKSTFCSDQIMGNILQNLKPC 467
427 KFLNKRGINLSEPKLGASQITVQSGEDGTETNFCSSDITVEENVLQSLYPC 477

I 15
-923-779-151
ence 151, Application US/09923779
nt No. US20020076721A1
RAL INFORMATION:
PLICANT: Pyle, Ruth A.
PLICANT: Xu, Jiangchun
PLICANT: Kalos, Michael D.
LE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
LE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
LE REFERENCE: 210121.553
RENT APPLICATION NUMBER: US/09/923,779
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

cleic - nucleic search, using sw model

n: January 6, 2004, 08:31:36 ; Search time 411 Seconds  
(without alignments)  
9221.438 Million cell updates/sec

US-10-038-517-1

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ng table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

hed: 2552756 seqs, 1349719017 residues

number of hits satisfying chosen parameters: 5105512

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um DB seq length: 2000000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

t	Score	Query Match	Length	DB	ID	Description
1	1404	100.0	1404	24	ABL59436	Nucleotide sequenc
2	1404	100.0	1422	24	ASN87363	Human lipase encod
3	1402.4	99.9	2352	22	RAD03848	Human lipase prote
4	1234.6	87.9	1383	24	AAD27797	Human pancreatic 1
5	1115.8	79.5	1526	24	ABL60540	Human lipid metabo
6	978.8	69.7	1389	24	ABA90354	Human polynucleoti
7	808	57.5	1540	24	ABN60002	Novel human coding
8	386.2	27.5	1481	24	ABL69985	Pancreas cancer re

9	353.8	25.2	1427	23	AAS81082	DNA encoding novel
10	342.6	24.4	1454	24	ABL59552	Human triacylglyce
11	342.6	24.4	1471	24	ABL44205	cDNA #145 encoding
12	342.6	24.4	1471	24	ABL69968	Pancreas cancer re
13	342.6	24.4	1536	21	ABL69880	Human pancreatic c
14	338	24.1	1410	23	AAS81083	DNA encoding novel
15	338	24.1	1450	24	ABL69986	Pancreas cancer re
16	338	24.1	1506	21	AAC99052	Human pancreatic c
17	334.8	23.8	1422	14	AAQ35064	GPL(+) mutant with
18	330.2	23.5	1404	14	AAQ35059	Human pancreatic 1
19	297.8	21.2	1206	21	AAC00081	Human secreted pro
20	276.4	19.7	1384	14	AAQ35058	Guinea pig pancrea
21	245	17.5	915	23	AAS83973	DNA encoding novel
22	245	17.5	915	23	AAS85111	DNA encoding novel
23	245	17.5	915	23	AAS91515	DNA encoding novel
24	245	17.5	1142	23	AAS89469	DNA encoding novel
25	234	16.7	878	22	AAI89392	Human polynucleoti
26	224	16.0	938	24	ABK44199	CDNA #139 encoding
27	209.2	14.9	907	24	ABK44136	CDNA #76 encoding
28	204.2	14.5	879	24	ABK44154	CDNA #94 encoding
29	203	14.5	963	24	ABK44082	CDNA #22 encoding
30	202.6	14.4	766	24	ABK44133	CDNA #73 encoding
31	198.8	14.2	872	24	ABK44164	CDNA #104 encoding
32	194.4	13.8	800	24	ABV95086	Human pancreatic c
33	192.6	13.7	789	24	ABV95051	Human pancreatic c
34	189.2	13.5	735	24	ABK44142	CDNA #82 encoding
35	188.6	13.4	633	21	AAC98794	Human pancreatic c
36	187	13.3	750	24	ABK44137	CDNA #77 encoding
37	186.2	13.3	764	24	ABK44138	CDNA #78 encoding
38	179.8	12.8	548	24	ABV97752	Human pancreatic c
39	179.8	12.8	567	24	ABV97965	Human pancreatic c
40	179.6	12.8	789	24	ABK44135	CDNA #75 encoding
41	179.4	12.8	599	24	ABV98006	Human pancreatic c
42	178.8	12.7	526	24	ABV97817	Human pancreatic c
43	178.8	12.7	780	24	ABK44145	CDNA #85 encoding
44	177.6	12.6	741	24	ABK44140	CDNA #80 encoding
45	175	12.5	761	24	ABK44134	CDNA #74 encoding

## ALIGNMENTS

RESULT 1  
ABL59436  
ID ABL59436 standard; cDNA; 1404 BP.

XX AC ABL59436;

XX XX 22-OCT-2002 (first entry)

XX DE Nucleotide sequence of a human lipase.

XX KW Human; lipase; enzyme; mental disorder; disease; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT CDS 1..1404  
FT FT /\*tag= a  
FT FT /product= "lipase"  
FT FT replace (378, G)  
FT FT /\*tag= b  
FT FT replace (1141, G)  
FT FT /\*tag= c  
FT FT /note= "this results in the mutation Ile381Val"  
FT FT replace (1144, A)  
FT FT /\*tag= d  
FT FT /note= "this results in the mutation Gly382Arg"

PN WO200253753-A2.

XX 11-JUL-2002.

XX

03--JAN-2002; 2002WO-US00223.

05-JAN-2001; 2001US-259830P.

(LEXI-) LEXICON GENETICS INC.

Yu X, Turner CA;

WPI; 2002-583623/62.

P-PSDB; ABB77987.

Nucleic acid molecule encoding a human lipase, useful in therapeutic, diagnostic and pharmacogenomic applications, as DNA markers for restriction fragment length polymorphism analysis and in forensic biology -

Claim 1; Page 35; 36pp; English.

The present sequence encodes a human lipase polypeptide. The lipase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenomic applications, and for identifying compounds that modulate, i.e., act as agonists or antagonists of the gene expression or gene product activity. They are also useful in the human lipase protein gene regulation and/or as antisense primers in amplification reactions of the nucleic acid sequences, for detecting mutant human proteins or inappropriately expressed proteins for the diagnosis of disease, for screening for drugs effective in treating the symptomatic or phenotypic manifestations of perturbing the normal function of the protein in the body, for generating transgenic animals and antibodies, for identifying other cellular gene products related to the protein, and as reagents in assays for screening for compounds that can be used as pharmaceutical agents in the therapeutic treatment of mental, biological or medical disorders and diseases.

Sequence 1404 BP: 413 A: 274 C: 303 G: 414 T: 0 other:

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ery Match      100.0%; Score 1404; DB 24; Length 1404;
st Local Similarity 100.0%; Pred. No. 0;
tches 1404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 GAGTTGGTAGGTTTACCCCTGGTCTCCAGAGAGAATAAACATCGTTCCTGCTCTACACT 180  
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121 GAGTTGGTAGGTTTACCCCTGGTCTCCAGAGAGAATAAACATCGTTCCTGCTCTACACT 180

181 ATACACAATCCCAATGCCATCAGGAGATCAGTGGGTTAAATCTTCAACTATCCAAGCC 240  
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181 ATACACAATCCCAATGCCATCAGGAGATCAGTGGGTTAAATCTTCAACTATCCAAGCC 240

241 TCATATTTGGAAACAGACACAGATCACCCGATCAACATAGCTGGATGGAACACAGATGCG 300

241 TCATATTTGGAAACAGACACAGATCACCCGATCAACATAGCTGGATGGAACACAGATGCG 300

301 AAATGGCAGAGAGACATGTGCAATGTGTTGCTACAGCTGGAAGATATAAAATTGCATTAT 360

361 TTAGATTGGATCAACGGTTTACCGGGAAATACATCCATGCTGTAAACAAATCTCCGGTGTGTT 420

421 GGTCCTGAGGTGGCTATTATTATTGATGTTCTCATGAAAAAAATTGAATATTCCTCCCTTCT 480

[illegible]

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541	ATACCAGGCCCTTGGAAATAAAGCTGGGTTGGACCCAGAGCTGGGCCATATTTTCCCAACAACACT	600
QY		
601	CCAAAGGAAGTCAGGCTAGACCCCTCGGATGCCAACCTTTGTGACGTTATTCATACAAAT	660
DB		
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QY		
661	GCAGCTCGCATCCTCTTTGAGCTTGGGTGGGTTGGAAACCATTTGATGCTTGTGGTCACTCTTGAC	720
DB		
661	GCAGCTCGCATCCTCTTTGAGCTTGGGTGGGTTGGAAACCATTTGATGCTTGTGGTCACTCTTGAC	720
QY		
721	TTTTTACCCAAATGAGGGGAAGCACATGCCAGGATGTGAAGACTTAAATTCACCTTTACTG	780
DB		
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QY		
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DB		
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QY		
841	CGAAGTTATCAATTTTATGCTGAAAGCATTCCTTAATCCTGATGCATTTATTTGCTTATCCT	900
DB		
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QY		
961	CCAAACAATGGGTGCAATTTTGTGATAGATTCTTCAAAATATGAAGACTAATGGATCA	1020
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1021	CATTATTTTTTAAACACAGGGTCCCTTTCCCATTTGCCCGTTGGAGGCACAAATGTCT	1080
DB		
1021	CATTATTTTTTAAACACAGGGTCCCTTTCCCATTTGCCCGTTGGAGGCACAAATGTCT	1080
QY		
1081	GTTAAACTAGTGGAAACGAGTCACCTCAAGAACTGTCTTCTTCGTGTAGCGGGGCA	1140
DB		
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QY		
1141	ATTGGGAAAACCTGGGAGTTTGCCATTGTCACTGGGAAAACCTTGAGCCAGGATGACTTAC	1200
DB		
1141	ATTGGGAAAACCTGGGAGTTTGCCATTGTCACTGGGAAAACCTTGAGCCAGGATGACTTAC	1200
QY		
1201	ACAAAAATTAATTCGATGCGAGTGTAACTGTTGAGAAACATTACAAGTGTTCAGTTCATCTGG	1260
DB		
1201	ACAAAAATTAATTCGATGCGAGTGTAACTGTTGAGAAACATTACAAGTGTTCAGTTCATCTGG	1260
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1261	AAAAACAATTTGTTGAGATGCTCAGATAGTTGGGAGCAGAAAAATGGGTGATAAATACA	1320
DB		
1261	AAAAACAATTTGTTGAGATGCTCAGATAGTTGGGAGCAGAAAAATGGGTGATAAATACA	1320
QY		
1321	TCTGGGAAATATGGATATAAATCTACTTCTGTAGCCAAAGACATTATGGGACCTTAATATT	1380
DB		
1321	TCTGGGAAATATGGATATAAATCTACTTCTGTAGCCAAAGACATTATGGGACCTTAATATT	1380
QY		
1381	CTCCAGAACCTGAAAACCATGCTAA	1404
DB		
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## RESULT 2

ABN87363

ID ABN87363 standard; cDNA; 1422 BP.

XX

AC ABN87363;

XX

DT 01-AUG-2002 (first entry)

DE Human lipase encoding cDNA sequence SEQ ID NO:1. XX

Human, lipase; enzyme; therapeutic; gene; ss.

Homo sapiens.

Key Location/Qualifiers  
 CDS 9..1412  
 /\*tag= a  
 /product= "lipase"

US2002052034-A1.

02-MAY-2002.

14-DEC-2000; 2000US-0735933

28-SEP-2000; 2000US-235925P

(GUEG/) GUEGLER K.  
 (WEBS/) WEBSTER M.  
 (KETC/) KETCHUM K A.  
 (DFRA/) DI FRANCESCO V.  
 (BEAS/) BEASLEY E M.

Guegler X, Webster M, Ketchum KA, Di Francesco V, Beasley EM;

WPI; 2002-443697/47.

P-PSDB; ABB79039.

A lipase protein identified from the human genome is related to the pancreatic lipase subfamily, and is useful to provide new drug targets in the discovery of therapeutics for lipase-mediated disease -

Claim 4; Fig 1; 85pp; English.

The present sequence encodes a human lipase protein. Molecules from the present invention can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate lipase activity in cells and tissues that express lipase. N.B. The present sequence has been given as a protein sequence in the Sequence Listing of the present invention, but if you put the protein sequence into single letter code you get the nucleotide sequence given in Fig 1.

Sequence 1422 BP; 418 A; 279 C; 306 G; 419 T; 0 other;

ry Match 100.0%; Score 1404; DB 24; Length 1422;

t Local Similarity 100.0%; Pred.No. 0;

ches 1404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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9 ATGCTGGAAATTGGATTGTTGCAATCTTGTCATCAAGGAAAGATT 68

61 TGTATGAAGGTTAGGTTGTTTCAAGATGTTTACCATGGACCAAGATTCTCAACA 120

69 TGTATGAAGGTTAGGTTGTTTCAAGATGTTTACCATGGACCAAGATTCTCAACA 128

121 GAGTGGTAGGTTTACCTGGTCTCAGAGAAGATAAACATCTGGTTCCTGCTCACT 180

129 GAGTGGTAGGTTTACCTGGTCTCAGAGAAGATAAACATCTGGTTCCTGCTCACT 188

181 ATACAAATCCCAATGCCCTATCAGGAGATCAGTGGGTTAATCTTCAACTATCCAGGCC 240

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241 TCATATTTGGAAACACAGAAGATCACCGTATCAACATAGCTGATGGAACAGATGGC 300

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 Db 1329 TCTGGAAATATGATATAAATCTACCTTCTGTAGCAAGACATTTATGGACCTAATTT 1388  
 QY 1381 CTCCAGACCTGAAACCATGCTAA 1404  
 Db 1389 CTCCAGACCTGAAACCATGCTAA 1412

LT 3

3848

AAD03848 standard; cDNA; 2352 BP.

AAD03848;

19-JUN-2001 (first entry)

Human lipase protein, MLip-1 cDNA.

Human; lipase; MLip-1; antiinflammatory; antilipemic; cardiant; therapy; anorectic; cholesterol biosynthesis; lipid metabolism; diabetes; obesity; pancreatic disorder; nutritional disorder; malabsorption; malnutrition; metabolic disorder; hyperlipidaemia; hypolipidaemia; abdominal lesion; lipidoses; pancreatic duct obstruction; Gaucher's disease; peritonitis; atherosclerosis; Niemann-Pick disease; arteriosclerosis; pancreatitis; coronary artery disease; perforated peptic ulcer; intestinal obstruction; linoleic acid deficiency; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 125..1528

/\*tag= a

/product= "Human lipase protein, MLip-1"

/note= "The coding region is specifically claimed

as SEQ ID NO:2 in claim 2 (page no: 80) of the

specification"

sig\_peptide 125..175

/\*tag= b

mat\_peptide 176..1525

/\*tag= c

/product= "Human mature lipase protein, MLip-1"

WO200125409-A1.

12-APR-2001.

02-OCT-2000; 2000WO-US27116.

01-OCT-1999; 99US-0411132.

(MILL-) MILLENIUM PHARM INC.

Khodadoust M, Kapeller-libermann R;

WPI: 2001-266302/27.

P-PSDB; AAE00508.

Novel isolated lipase, MLip-1, useful for identifying compounds which modulate MLip-1 activity, for treating conditions or disorders associated with aberrant activity of MLip-1 such as hypolipidemia, obesity

Claim 2; Page 95-96; 112pp; English.

The present sequence is human lipase protein, MLip-1 cDNA. MLip-1 catalyses the formation and cleavage of ester bonds between fatty acyl moieties and glyceride moieties. It is involved in dietary fat degradation and absorption, cholesterol biosynthesis and maintenance of plasma lipid and lipoprotein levels. MLip-1 is also useful for identifying compounds which modulates its activity and expression. These compounds are useful for preventing, diagnosing or treating disorders relating to inappropriate lipid metabolism and aberrant pancreatic function such as diabetes, obesity, nutritional disorders (e.g. lipid malabsorption and malnutrition), metabolic disorders (particularly including lipid metabolism anomalies such as hyperlipidaemia of types I to V and hypolipidaemia), pancreatitis, obstruction of the pancreatic duct, various lipidoses (e.g. Gaucher's disease and Niemann-Pick disease), atherosclerosis, arteriosclerosis, coronary artery disease, perforated peptic ulcer, abdominal lesions, intestinal obstruction,

CC peritonitis and linoleic acid deficiency. MLip-1 and its modulators can be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing and forensic biology assays), predictive medicine (e.g. CC diagnostic assays, prognostic assays, monitoring of clinical trials and pharmacogenomic applications) and methods of treatment (e.g. therapeutic CC and prophylactic methods).

XX Sequence 2352 BP; 705 A; 431 C; 491 G; 722 T; 3 other;

Query Match	99.9%;	Score 1402.4;	DB 22;	Length 2352;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1403;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

  

Qy	1	ATGCTTGAATTTGGATTGTTGTCATTCTTTTGGCACATCAAGAGGAAAAAGATT	60
Ds	125	ATGCTTGAATTTGGATTGTTGTCATTCTTTTGGCACATCAAGAGGAAAAAGATT	184
Qy	61	TGCTATGAAGTTAGGTTGTTTCAAGATGGTTTACCATGACACAGGACTTTCTCAACA	120
Ds	185	TGCTATGAAGTTAGGTTGTTTCAAGATGGTTTACCATGACACAGGACTTTCTCAACA	244
Qy	121	GAGTTGGTAGGTTTACCTTGGTCTCCAGAGAGATAAACAACATCGTTTCCCTGCTTACACT	180
Ds	245	GAGTTGGTAGGTTTACCTTGGTCTCCAGAGAGATAAACAACATCGTTTCCCTGCTTACACT	304
Qy	181	ATACACATCCCAATGCTTATCAGGAGATCAGTGGGTTAATCTTCAACTATCCAGCC	240
Ds	305	ATACACATCCCAATGCTTATCAGGAGATCAGTGGGTTAATCTTCAACTATCCAGCC	364
Qy	241	TCATATTTTGGAAACAGACAGATCACCCGTTATCAACATAGCTGGATGGAACACAGATGC	300
Ds	365	TCATATTTTGGAAACAGACAGATCACCCGTTATCAACATAGCTGGATGGAACACAGATGC	424
Qy	301	AAATGGCAGAGACATGTGCAATGTGTTGCTACAGCTGGAAGATATAAATTGCAATTAAT	360
Ds	425	AAATGGCAGAGACATGTGCAATGTGTTGCTACAGCTGGAAGATATAAATTGCAATTAAT	484
Qy	361	TTAGATTGGATCAACGGTTTCAAGGAAATACATCCATGCTGTAAACAATCTCGTGTGTT	420
Ds	485	TTAGATTGGATCAACGGTTTCAAGGAAATACATCCATGCTGTAAACAATCTCGTGTGTT	544
Qy	421	GGTGTGAGTGGCTTATTTTATGATGTTCTCATGAAATAAATTTGAATATTCCCTTCT	480
Ds	545	GGTGTGAGTGGCTTATTTTATGATGTTCTCATGAAATAAATTTGAATATTCCCTTCT	604
Qy	481	AAATGTCACATTGATTCGCCACACAGCTTGGGAGACACCTGGCTGGGGAGAGCTGGTCAAGG	540
Ds	605	AAATGTCACATTGATTCGCCACACAGCTTGGGAGACACCTGGCTGGGGAGAGCTGGTCAAGG	664
Qy	541	ATACAGGCTTGGAAAGATAAATCTGGGTTGGACCCAGCTGGGCCATTTTCCACAACT	600
Ds	665	ATACAGGCTTGGAAAGATAAATCTGGGTTGGACCCAGCTGGGCCATTTTCCACAACT	724
Qy	601	CCAAAGGAGTCAAGCTAGACCCCTCGGATGCCAATTTGTTGAGTTATTTCATCAAT	660
Ds	725	CCAAAGGAGTCAAGCTAGACCCCTCGGATGCCAATTTGTTGAGTTATTTCATCAAT	784
Qy	661	GCAGCTCGCATCTCTTTGAGCTTGGTGTGGAACCATTTGCTGTGGTCACTTTCAC	720
Ds	785	GCAGCTCGCATCTCTTTGAGCTTGGTGTGGAACCATTTGCTGTGGTCACTTTCAC	844
Qy	721	TTTTACCCAAATGGAGGAGACATGCCAGGATGGAAGACTTAATTACACCTTTACTG	780
Ds	845	TTTTACCCAAATGGAGGAGACATGCCAGGATGGAAGACTTAATTACACCTTTACTG	904
Qy	781	AAATTTAACTTCAATCTTACAAAAGAAATGGCTTCTCTTTGACTGTAAACCATGCC	840
Ds	905	AAATTTAACTTCAATCTTACAAAAGAAATGGCTTCTCTTTGACTGTAAACCATGCC	964
Qy	841	CGAAGTTATCAATTTTATGCTGAAAGCAATCTTAATCTGATGCAATTTATGCTTATCCT	900
Ds	965	CGAAGTTATCAATTTTATGCTGAAAGCAATCTTAATCTGATGCAATTTATGCTTATCCT	1024

901 TGAGATCCCTACATCTTTTAAAGCAGGAAATGCTCTTTTGTTCACAAAGAGTTGC 960  
 1025 TGAGATCCCTACATCTTTTAAAGCAGGAAATGCTCTTTTGTTCACAAAGAGTTGC 1084  
 961 CCAACAATGGGTGATTTGGTGTGATAGATTTCACTTCAAAAATATGAAGACTAATGGATCA 1020  
 1085 CCAACAATGGGTGATTTGGTGTGATAGATTTCACTTCAAAAATATGAAGACTAATGGATCA 1144  
 1021 CATTATTTTAAACACAGGTCCTTTTCCCATTTGCCGTTGGAGGACAGAAATGTC 1080  
 1145 CATTATTTTAAACACAGGTCCTTTTCCCATTTGCCGTTGGAGGACAGAAATGTC 1204  
 1081 GTTAACTAGTGAAGCGAAGTCACTCAAGGAAGTGTCTTCTCGTGTAGCGGGGCA 1140  
 1205 GTTAACTAGTGAAGCGAAGTCACTCAAGGAAGTGTCTTCTCGTGTAGCGGGGCA 1264  
 1141 ATTGGGAACCTGGGAGTTTGCATGTCTAGTGTGAGGAGCAAGTGTGATGAATAACA 1200  
 1265 ATTGGGAACCTGGGAGTTTGCATGTCTAGTGTGAGGAGCAAGTGTGATGAATAACA 1324  
 1201 AAAAAATTAATCGATGCAATGTTTAAAGTGTGGAACATTTACAAAGTGTTCAGTTCACTCGG 1260  
 1325 AAAAAATTAATCGATGCAATGTTTAAAGTGTGGAACATTTACAAAGTGTTCAGTTCACTCGG 1384  
 1261 AAAAAATTTGTTGAAGATTTGCAATGTCTAGTGTGAGGAGCAAGTGTGATGAATAACA 1320  
 1385 AAAAAATTTGTTGAAGATTTGCAATGTCTAGTGTGAGGAGCAAGTGTGATGAATAACA 1444  
 1321 TCTGGGAATATGATGAATAAATCTACTCTCTGTAGTGTGAGGAGCAAGTGTGATGAATAACA 1380  
 1445 TCTGGGAATATGATGAATAAATCTACTCTCTGTAGTGTGAGGAGCAAGTGTGATGAATAACA 1504  
 1381 CTCGAGAACTGAAACCTGCTAA 1404  
 1505 CTCGAGAACTGAAACCTGCTAA 1528

T 4

797

AAD27797 standard; DNA; 1383 BP.

AAD27797;

18-APR-2002 (first entry)

Human pancreatic lipase gene, sbg237163LIPASE.

Human; therapy; wound healing disorder; vaccine; cancer; infection; autoimmune disorder; haematopoietic disorder; inflammation; arthritis; Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic; multiple sclerosis; Alzheimer's disease; analgesic; cardiasthma; ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain failure; depression; cardiovascular disease; myocardial infarction; renal failure; respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder; type II diabetes mellitus; skeletal muscle disorder; immunosuppressive; hyperplenism; renal disease; hypoglycaemia; gastrointestinal disease; neoptropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory; haemostatic; vulvar; anticonvulsant; antineoplastic; neuroprotective; nephrotoxic; hypotensive; vasotrophic; cytostatic; cerebroprotective; allergy; pancreatic lipase; gene; ds.

Homo sapiens.

Key Location/Qualifiers

CD5 1..1383

/tag= a

/product= "Human pancreatic lipase"

/note= "CDS does not include stop codon"

/partial

W0200198342-A1.

27-DEC-2001.

XX 22-JUN-2001; 2001WO-US19929.  
 XX 22-JUN-2000; 2000US-213156P.  
 XX 22-JUN-2000; 2000US-213161P.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;  
 XX Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;  
 XX WPI; 2002-139783/18.  
 XX P-PSDB; AAE17302.  
 XX Novel secreted and membrane-associated polypeptides and polynucleotides useful for preventing, ameliorating or correcting dysfunction or disease including diabetes, cancer, hypertension and growth abnormalities  
 XX Claim 2; Page 83; 138pp; English.  
 XX The invention relates to secreted and membrane-associated polypeptides and polynucleotides. The sequences of the invention are useful in diagnostic assays for detecting diseases associated with inappropriate activity or levels of these polynucleotides, and in identifying their agonists and antagonists that are potentially useful in therapy. The sequences of the invention are useful as vaccines for inducing immunological response. The sequences of the invention are useful for treating cancers, infections, autoimmune disorders, haematopoietic disorders, wound healing disorders, cholesteryl ester storage disease, inflammation, congenital muscular dystrophy, junctional epidermolysis bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis, viral and bacterial infections, Alzheimer's disease, asthma, arthritis, allergies, schizophrenia, sbg44245FOA-associated disorders, septicemia, psoriasis, inflammatory bowel disease, transplant rejection, graft versus host disease, ischaemia, stroke, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis, brain disorders including paraspranuclear palsy, myotonic dystrophy, depression, anxiety disorders and sleep disorders, cardiovascular diseases including congestive heart failure and myocardial infarction, respiratory diseases including chronic obstructive pulmonary disease, acute bronchitis and adult respiratory distress syndrome, liver disorders including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral and non-viral hepatitis, type II diabetes mellitus, renal disease including acute and chronic renal failure, glomerulonephritis, Fanconi's syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia and tendinitis, gastrointestinal diseases including intestinal obstruction and tropical sprue, spleen disorders including hyperplenism, Hodgkin's disease and malignant lymphoma, testicular cancer, male reproductive diseases including low testosterone and male infertility. The present sequence is human pancreatic lipase gene.  
 XX Sequence 1383 BP; 399 A; 268 C; 302 G; 414 T; 0 other;  
 SQ Query Match 87.9%; Score 1234.6; DB 24; Length 1383;  
 Best Local Similarity 93.8%; Pred. No. 0;  
 Matches 1314; Conservative 0; Mismatches 69; Indels 18; Gaps 2;  
 QY 1 ATGCTTGGAATTTGGATTGTTCATTTCTGTTTGGCACATCAAGAGAAAGAGTT 60  
 Db 1 ATGCTTGGAATTTGGATTGTTCATTTCTGTTTGGCACATCAAGAGAAAGAGTT 60  
 QY 61 TCGTATGAAGGTTAGGGTGTTCAAAGATGGTTTACCATGGACAGGACTTTCTCAACA 120  
 Db 61 TCGTATGAAGGTTAGGGTGTTCAAAGATGGTTTACCATGGACAGGACTTTCTCAACA 120  
 QY 121 GAGTTGGTAGGTTTACCTGTCTCCAGAGAGTAACACTCGTTTCTGCTCTACT 180  
 Db 121 GAGTTGGTAGGTTTACCTGTCTCCAGAGAGTAACACTCGTTTCTGCTCTACT 180  
 QY 181 ATACACATCCCAATGCCTATCAGGAGATCAGTGCGGTTAAATTTCTCACTATCCAAGCC 240

181 ATACAAATCCCAATGCGTATCAGAGATCAGTGGTAAATCTTCAATATCCAAAGCC 240  
 241 TCATATTTTGGAAACAGACAGATCACCAGTATCAACATAGCTGGATGGAAACAGATGGC 300  
 241 TCATATTTTGGAAACAGACAGATCACCAGTATCAACATAGCTGGATGGAAACAGATGGC 300  
 301 AAATGGCAGAGAGACATGTGCAATGTGTGCTACAGCTGGAAGATATAAATTCATTAAT 360  
 301 AAATGGCAGAGAGACATGTGCAATGTGTGCTACAGCTGGAAGATATAAATTCATTAAT 360  
 361 TTAGATTTGATCAACGGTTACGGGAATACATCTGTAAACATCTCCGTGTGTT 420  
 361 TTAGATTTGATCAACGGTTACGGGAATACATCTGTAAACATCTCCGTGTGTT 420  
 421 GGTGCTGAGTGGCTTATTTTATTGATGTTCTCATGAAAAAATTTGAATATCCCTTCT 480  
 421 GGTGCTGAGTGGCTTATTTTATTGATGTTCTCATGAAAAAATTTGAATATCCCTTCT 480  
 481 AAATGCACTGATTTGGCCACAGCTTGGGACACACCTGCTGGGAGCTGGGTCAAGG 540  
 481 AAATGCACTGATTTGGCCACAGCTTGGGACACACCTGCTGGGAGCTGGGTCAAGG 540  
 541 ATACAGGCGCTTGAAGAAATAACTGGGTGGACCCAGCTGGGCCATTTTCCACAACT 600  
 541 ATACAGGCGCTTGAAGAAATAACTGGGTGGACCCAGCTGGGCCATTTTCCACAACT 600  
 601 CCAAGGAAGTACAGCTAGACCTTCGGATGCCAACTTTGTTGACGTTATTCATAAAT 660  
 601 CCAAGGAAGTACAGCTAGACCTTCGGATGCCAACTTTGTTGACGTTATTCATAAAT 660  
 661 GCAGCTCGCATCTCTTTGAGCTTGGTGTGGAAACCATTTGATGTTGGTCACTTTGAC 720  
 661 GCAGCTCGCATCTCTTTGAGCTTGGTGTGGAAACCATTTGATGTTGGTCACTTTGAC 720  
 721 TTTTACCAATGGAGGAACACATCCAGATGTGAAGACTTAATACACCTTTACTG 780  
 721 TTTTACCAATGGAGGAACACATCCAGATGTGAAGACTTAATACACCTTTACTG 780  
 781 AAATTTAACTTCAATGCTTACAAAAAGAAATGCTTCTTCTGACTGTACCAATGCC 840  
 781 AAATTTAACTTCAATGCTTACAAAAAGAAATGCTTCTTCTGACTGTACCAATGCC 840  
 841 CGAAGTTATCAATTTTATGCTGAAAGCATTTTAACTCTGATGCAATTTATGCTTATCT 900  
 841 CGAAGTTATCAATTTTATGCTGAAAGCATTTTAACTCTGATGCAATTTATGCTTATCT 900  
 901 TGTAGATCTACATCTTTTAAAGCAGAAATGCTTCTTTTGTCCAAAGAGTGTGC 960  
 901 TGTAGATCTACATCTTTTAAAGCAGAAATGCTTCTTTTGTCCAAAGAGTGTGC 960  
 961 CCAACAAATGGGTCAATTTTGTCTGATAGATTTTCACTTCAAAAAATATGAAGACTAATGGATCA 1020  
 961 CCAACAAATGGGTCAATTTTGTCTGATAGATTTTCACTTCAAAAAATATGAAGACTAATGGATCA 1020  
 1021 CATTATTTTAAACACAGGTGCTTCCCATTTGCCGTTGGAGGACCAAAATGCTT 1080  
 1021 CATTATTTTAAACACAGGTGCTTCCCATTTGCCGTTGGAGGACCAAAATGCTT 1080  
 1014 CCGTTTCTCTT-----CTTGTTTCTTATATCTAGTTTGGAGGACCAAAATGCTT 1062  
 1014 CCGTTTCTCTT-----CTTGTTTCTTATATCTAGTTTGGAGGACCAAAATGCTT 1062  
 1081 GTTAACTCAGTGGAGGAGTCACTCAAGGACTGCTTCTTCTGTTAGGCGGGCA 1140  
 1081 GTTAACTCAGTGGAGGAGTCACTCAAGGACTGCTTCTTCTGTTAGGCGGGCA 1140  
 1063 GTTAACTCAGTGGAGGAGTCACTCAAGGACTGCTTCTTCTGTTAGGCGGGCA 1122  
 1141 ATTGGAAATCTGGAGTTTGGCATTGTCACTGGAATACTTGGAGGAGGATGCTTAC 1200  
 1123 GTTAGGAAATCTGGAGTTTGGCATTGTCACTGGAATACTTGGAGGAGGATGCTTAC 1182  
 1201 ACAAAATTAATGATGAGATGTTAACTGGAAACATTAAGTGTTCAGTTCATCTGG 1260  
 1183 ACAAAATTAATGATGAGATGTTAACTGGAAACATTAAGTGTTCAGTTCATCTGG 1242  
 1261 AAAAAACATTTGTTTGAAGATTTCTCAGAAATAGTTGGGAGCAGAAATGGTATAATACA 1320  
 1261 AAAAAACATTTGTTTGAAGATTTCTCAGAAATAGTTGGGAGCAGAAATGGTATAATACA 1320

1243 AAAAAACATTTGTTTGAAGATTTCTCAGAAATAGTTGGGAGCAGAAATGGTATAATACA 1302  
 1321 TCTGGAAATATGATATAAATCTACCTTCTGTAGCCAAGACATTTATGGACCTATATT 1380  
 1303 TCTGGAAATATGATATAAATCTACCTTCTGTAGCCAAGACATTTATGGACCTATATT 1362  
 1391 CTCAGAACCTGAAACCATGC 1401  
 1363 CTCAGAACCTGAAACCATGC 1383

RESULT 5  
 ASL60540  
 ID ABL60540 standard; cDNA; 1526 BP.  
 AC ABL60540;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human lipid metabolism enzyme (LME)-4 cDNA (clone id: 7482937CB1).  
 XX  
 KW Human; lipid metabolism enzyme; LME; cytostatic; neuroprotective; gene;  
 KW nontropic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;  
 KW antisclerotic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;  
 KW gene therapy; protein therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 259..1365  
 FT /\*tag= a  
 FT /product= "lipid metabolism enzyme"  
 FT /note= "LME-4"  
 XX  
 FN WO200229036-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 05-OCT-2001; 2001WO-US31302.  
 XX  
 PR 06-OCT-2000; 2000US-238388P.  
 PR 13-OCT-2000; 2000US-240616P.  
 PR 02-NOV-2000; 2000US-245719P.  
 PR 08-NOV-2000; 2000US-247503P.  
 PR 17-NOV-2000; 2000US-249503P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Hazland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;  
 PI Wallia NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;  
 PI Lal PG, Tribouley CM;  
 XX  
 DR WPI: 2002-315862/35.  
 DR P-PSDB: ABB08004.  
 XX  
 PT Lipid Metabolism Enzymes and nucleic acids, useful for preventing,  
 PT diagnosing and treating e.g. cancer, Alzheimer's disease and  
 PT Creutzfeld-Jakob disease -  
 XX  
 PS Claim 5; Page 123; 127pp; English.  
 CC  
 CC The invention relates to human lipid metabolism enzymes (LMEs) and  
 CC encoding polynucleotides. The LMEs can be expressed by standard  
 CC recombinant technology. The LME polypeptides, polynucleotides and  
 CC modulators may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate LME expression such as cancer  
 CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.  
 CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections  
 CC (e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome  
 CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina  
 CC pectoris and mitral valve prolapse). The present sequence represents the  
 CC human LME-4 encoding cDNA.

Sequence 1526 BP; 440 A; 303 C; 325 G; 458 T; 0 other;

ry Match 79.5%; Score 1115.8; DB 24; Length 1526;  
t Local Similarity 94.3%; Pred. No. 4.8e-305;  
ches 1198; Conservative 0; Mismatches 2; Indels 71; Gaps 1;  
205 GAGATCAGTGGCGTTAAATTCCTCAACTATCCAGGCTCATATTTTGGACAGACAGATC 264  
|||||  
95 GAGATCAGTGGCGTTAAATTCCTCAACTATCCAGGCTCATATTTTGGACAGACAGATC 154  
|||||  
265 ACCGTTATCAACATAGCTGGATGGAAACACAGATGCCAAATGGCAGAGAGACATGTGCAAT 324  
155 ACCGTTATCAACATAGCTGGATGGAAACACAGATGCCAAATGGCAGAGAGACATGTGCAAT 214  
325 -----  
215 GTATGACATGAATAAGCTCCTTTTACACTAGCATCGAGCTTTATGTTTAACTGAATG 274  
325 -----GTGTTGCTACAGCTGGAAGATATATAATTCATTAAATTTAGATTGGATCA 373  
275 TACTTTGCAAGGTGTTGCTACAGCTGGAGATATATAATTCATTAAATTTAGATTGGATCA 334  
374 ACGGTTACGGGAATACATCCATGCTGTAACAATCTCCGTTGTTTGGTCTGAGGTGG 433  
335 ACGGTTACGGGAATACATCCATGCTGTAACAATCTCCGTTGTTTGGTCTGAGGTGG 394  
434 CTTATTTTATGATGTTCTCATGAAATAATTTGAATATTCCTCTTCAAAGTGCACCTTGA 493  
395 CTTATTTTATGATGTTCTCATGAAATAATTTGAATATTCCTCTTCAAAGTGCACCTTGA 454  
494 TTGGCCACAGCTTTGGGAGCACACCTCGGCTGGGGAAGCTGGCTCAAGATACACAGGCCCTTG 553  
455 TTGGCCACAGCTTTGGGAGCACACCTCGGCTGGGGAAGCTGGCTCAAGATACACAGGCCCTTG 514  
554 GAAGATAACTGGTTGAGCCAGCTGGGCCATTTTCCACAACTCCAAAGGAAGTCA 613  
515 GAAGATAACTGGTTGAGCCAGCTGGGCCATTTTCCACAACTCCAAAGGAAGTCA 574  
614 GGCTAGACCCCTCGATGCGCACTTTGTTGAGCTTATTTCATACAAATGCGAGTCGCATCC 673  
575 GGCTAGACCCCTCGATGCGCACTTTGTTGAGCTTATTTCATACAAATGCGAGTCGCATCC 634  
674 TCTTTGAGCTTGGTTGGAACCAATGATGTTGGTCACTTTGACTTTTACCTGAAATTTTAACTTCA 733  
635 TCTTTGAGCTTGGTTGGAACCAATGATGTTGGTCACTTTGACTTTTACCTGAAATTTTAACTTCA 694  
734 GAGGGAAGCACATGCCAGATGTAAGACTTAATTCACCTTTTACTGAAATTTTAACTTCA 793  
695 GAGGGAAGCACATGCCAGATGTAAGACTTAATTCACCTTTTACTGAAATTTTAACTTCA 754  
794 ATGCTTTACAAAAGAAATGGCTTCTTTGACTGTAACCATGCCCGAAGTTATCAAT 853  
755 ATGCTTTACAAAAGAAATGGCTTCTTTGACTGTAACCATGCCCGAAGTTATCAAT 814  
854 TTTATGCTGAAAGCACTTTAATCTCGATGCAATTTATGCTTATCTTGTAGATCCTTACA 913  
815 TTTATGCTGAAAGCACTTTAATCTCGATGCAATTTATGCTTATCTTGTAGATCCTTACA 874  
914 CATCTTTTAAAGCAGAAATTCCTTCTTTGTTCCAAAGAGGTTGCCCAATGGGTC 973  
875 CATCTTTTAAAGCAGAAATTCCTTCTTTGTTCCAAAGAGGTTGCCCAATGGGTC 934  
974 ATTTGCTGATAGATTTCACTTTCAAAAATATGAAGACTTAATGGAATCACTATTTTAA 1033  
935 ATTTGCTGATAGATTTCACTTTCAAAAATATGAAGACTTAATGGAATCACTATTTTAA 994  
1034 ACACAGGTCCTTCCCATTTGCTTCTTGGGCAAAATTCCTGTTAAACTCAGTG 1093  
995 ACACAGGTCCTTCCCATTTGCTTCTTGGGCAAAATTCCTGTTAAACTCAGTG 1054  
1094 GAAGCGAAGTCACTCAAGGAAGTCTTTTCTTCTGTTAGGGGGGCAATTTGGGAAACTG 1153  
1055 GAAGCGAAGTCACTCAAGGAAGTCTTTTCTTCTGTTAGGGGGGCAATTTGGGAAACTG 1114

QY 1154 GGGAGTTTGGCATTGTTCAGTGGAAAACTTGAGCCAGGCACTTACACAAAATTAATCG 1213  
Db 1115 GGGAGTTTGGCATTGTTCAGTGGAAAACTTGAGCCAGGCACTTACACAAAATTAATCG 1174  
QY 1214 ATGCAGATGTTAAAGTTGGAAACATTTACAGTGTTCAGTTCACTTGGAAAAACATTTGT 1273  
Db 1175 ATGCAGATGTTAAAGTTGGAAACATTTACAGTGTTCAGTTCACTTGGAAAAACATTTGT 1234  
QY 1274 TTGAAGATTTCTCAGAAATAAGTTGGGAGCAGAAAAATGGTCAATAATACATCTGGGAAATATG 1333  
Db 1235 TTGAAGATTTCTCAGAAATAAGTTGGGAGCAGAAAAATGGTCAATAATACATCTGGGAAATATG 1294  
QY 1334 GATATAATCTACCTTCTGTAGCCAGACATTTATGGGACCTATATTTCTCCAGAACCTGA 1393  
Db 1295 GATATAATCTACCTTCTGTAGCCAGACATTTATGGGACCTATATTTCTCCAGAACCTGA 1354  
QY 1394 AACCATGCTAA 1404  
Db 1355 AACCATGCTAA 1365  
RESULT 6  
ABA90354  
ID ABA90354 standard; cDNA; 1389 BP.  
XX ABA90354;  
AC ABA90354;  
XX  
DT 12-FEB-2002 (first entry)  
XX  
DE Human polynucleotide #29.  
XX  
KW Human; nootropic; neuroprotective; anticonvulsant; antidepressant;  
neuroleptic; tranquiliser; antiarrhythmic; cardiac; antischismatic;  
antiinflammatory; antilipemic; hepatotropic; virucide; antidiabetic;  
nephrotropic; anorectic; cytostatic; vaccine; neurological disease;  
cardiovascular disease; respiratory disease; liver disease;  
renal disease; skeletal muscle disease; gastrointestinal disease;  
placental disease; testicular cancer; male fertility; pancreatic disease;  
85.  
XX Homo sapiens.  
OS  
XX  
PN WO200181363-A1.  
XX  
PD 01-NOV-2001.  
XX  
PF 26-APR-2001; 2001WO-US13360.  
XX  
PR 27-APR-2000; 2000US-199963P.  
PR 11-MAY-2000; 2000US-203336P.  
PR 25-MAY-2000; 2000US-207087P.  
PR 26-MAY-2000; 2000US-207546P.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Agarwal P, Murdock PR, Rizvi SK, Smith RP, Xiang Z, Kabnick KS;  
PI Lai Y, Xie Q;  
XX  
XX WPI; 2002-041392/05.  
DR P-PSDB; ABB53289.  
XX  
XX Novel polypeptides and polynucleotides useful as a vaccine for  
preventing and treating diseases associated the polypeptide, e.g.  
PT Alzheimer's disease, dyslipidemia, obesity, diabetes, infertility,  
PT asthma, amnesia  
XX  
XX Claim 2; Page 60-61; 116pp; English.  
XX  
CC The invention relates to an isolated polypeptide comprising a 277, 480,  
583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1036,  
844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,

784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as given in the specification. The polypeptides, modulators of the polypeptides and antibodies against the polypeptides are useful for treating diseases such as neurological and psychiatric diseases including Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic dystrophy, anorexia and depression; cardiovascular diseases including congestive heart failure, Hodgkin's disease and myocardial infarction; respiratory diseases including asthma, chronic obstructive pulmonary disease, cystic fibrosis and adult respiratory distress syndrome; liver diseases including hypercholesterolaemia, cirrhosis, viral and nonviral hepatitis, Type II diabetes mellitus, and impaired glucose tolerance; renal disease including renal failure, acute tubular necrosis and glomerulonephritis; skeletal muscle diseases including Eulenburg's disease, hypoglycaemia and obesity; gastrointestinal diseases including myotonia congenita and intestinal obstruction; lymph diseases including lymphaglectasia; diseases of placenta including choriocarcinoma; diseases of testes including testicular cancer, male reproductive diseases including low testosterone and male infertility; and disease of pancreas including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The present sequence encodes a polypeptide of the invention.

Sequence 1389 BP; 392 A; 294 C; 304 G; 399 T; 0 other;  
 ery Match 69.7%; Score 978.8; DB 24; Length 1389;  
 st Local Similarity 82.6%; Pred. No. 2.6e-266;  
 tches 1137; Conservative 0; Mismatches 227; Indels 12; Gaps 1;

29 TGTCTTTGGCAATCAAGAGAAAGAGTTTCTATGAAGTTAGGGTGTTCAAAG 88  
 25 TGCTCTGGGAGCAGTAGCAGGAAAGAGTTTCTACGAAAGACTCGGTGTTCAGTG 85  
 89 ATGGTTTACCATGACAGGAGTTTCTACAGAGTTGGTAGTTTACCTGTCTCCAG 148  
 86 ATGACTCCCATGGTTCAGAAATACGGAAGACCCCTCCATATTTGCTGTGTCTCCAA 145  
 149 AGAAGATAAACAATCTGTTTCTGCTCTACATATACATATCCCAATGCCATATCAGGAGA 208  
 146 AAGATGTCAACACCCGCTCTCTATATACTAATGAGAACCCCAACAACTTCAAGAGA 205  
 209 TCAGTGGGTTAATTTCTCACTATCCAGCTCATATTTTGGACAGACAGATCACCC 268  
 206 TCAGTGGGTTAATTTCTCACTATCCAGCTCATATTTTGGACAGACAGATCACCC 265  
 269 GTATCAACATAGCTGGATGAAACACAGATGCCAATGCCAGAGACATGTGCAATGTGT 328  
 266 GTATCAACATAGCTGGATGAAACACAGATGCCAATGCCAGAGACATGTGCAATGTGT 325  
 329 TGCTACAGCTGGAAGATATAATTTGCAATATTTAGATTCGATCAACGGTTACGGGAAT 388  
 326 TGCTACAGCTGGAAGATATAATTTGCAATATTTAGATTCGATCAACGGTTACGGGAAT 385  
 389 ACATCCATGCTCTAAACAATCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 448  
 386 ACATCCATGCTCTAAACAATCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 445  
 449 TTCTCATGAAAAAATTTGAATATTTCCCTTTCTAAAGTGCACTGTGATGGCCACAGCTTG 508  
 446 TTCTCATGAAAAAATTTGAATATTTCCCTTTCTAAAGTGCACTGTGATGGCCACAGCTTG 505  
 509 GAGCACCTGCTGGGAGCTGGTTCAGGATACAGGACCCCTGGAGATTAACCTGGGT 568  
 506 GAGCACCTGCTGGGAGCTGGTTCAGGATACAGGACCCCTGGAGATTAACCTGGGT 565  
 569 TGGACCCAGCTGGGCAATTTTTCACACACTCCAAAGGAAGTCAGGCTAGACCCCTCGG 628  
 566 AGCATGCCCTGCGAGTTGGGCTGGAGTGTGCAACCGAGGGCTACCTGTATCTGCTACTC 625  
 629 ATGCCAATTTGTTGACGCTTATTCATACAAATCAGAGCTCGATCCCTCTTTGAGCTTGGTG 688  
 626 TGGCTAACAAATGTCAACTTCGTAGTACAAATCAGATGGATGCAACTCCCATTAATCCGCC 685  
 689 TTGGAACCAATGATGCTGT 748

Db 686 AGTGGATGAGGGGCACTTCGGGAACCCAGTAACCCCTCTCTGTACTCTCTCTGTCT 745  
 Qy 749 CAGGATGTGAGACTTAATTAACACCTTTACTGAAATTTAACTTCAATGCTTACAAAAAG 808  
 Db 746 TATGGTGGGTGATCTGGCTGGTCTCACTCGTATGTTTGGGCT-----G 793  
 Qy 809 AAATGGCTTCTTCTTCTTACTGTAAACCATGCCGGAAGTTATCAATTTTATGCTGAAAGCA 868  
 Db 794 AAATGGCTTCTTCTTCTTACTGTAAACCATGCCGGAAGTTATCAATTTTATGCTGAAAGCA 853  
 Qy 869 TTCTTAATCTGATGATTTATTTGCTTATCTTCTGTAGATCTTCTTCTTCTTCTTCTTCT 928  
 Db 854 TTCTTAATCTGATGATTTATTTGCTTATCTTCTGTAGATCTTCTTCTTCTTCTTCTTCT 913  
 Qy 929 GAAATGCTTCTTCTTCTTCTTCAAAAGAGGTTGCCCAACATGGGTCAATTTTCTGCTAGAT 988  
 Db 914 GAAATGCTTCTTCTTCTTCTTCAAAAGAGGTTGCCCAACATGGGTCAATTTTCTGCTAGAT 973  
 Qy 989 TTCACTTCAAAAATATGAAGACTTAATGATCAATTTTCTTCTTCTTCTTCTTCTTCTTCT 1048  
 Db 974 TTCACTTCAAAAATATGAAGACTTAATGATCAATTTTCTTCTTCTTCTTCTTCTTCTTCT 1033  
 Qy 1049 CCCATTTGCCGTTGGAGGCACAAATTTCTGTTAACTCAGTGGAGCGAAGTCACTC 1108  
 Db 1034 CCCATTTGCCGTTGGAGGCACAAATTTCTGTTAACTCAGTGGAGCGAAGTCACTC 1093  
 Qy 1109 AAGAACTGCTTCTTCTTCTTCTGAGGCGGCAATTTGGGAAACTCTGGGAGTTTGGCAATG 1168  
 Db 1094 AAGAACTGCTTCTTCTTCTTCTGAGGCGGCAATTTAGGAAACTCTGGGAGTTTGGCAATG 1153  
 Qy 1169 TCAGTGGAAACTTGGAGCGGCAATTTAGGAAACTCTGGGAGTTTGGCAATG 1228  
 Db 1154 TCAGTGGAAACTTGGAGCGGCAATTTAGGAAACTCTGGGAGTTTGGCAATG 1213  
 Qy 1229 TTGAAACATTAACAAGTGTTCAGTTCATCTGGAACCAATTTGTTGAGATTTCTCAGA 1288  
 Db 1214 TTGAAACATTAACAAGTGTTCAGTTCATCTGGAACCAATTTGTTGAGATTTCTCAGA 1273  
 Qy 1289 ATAGTTTGGAGCAGAAATGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1348  
 Db 1274 ATAGTTTGGAGCAGAAATGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1333  
 Qy 1349 TCTGTAGCCCAAGACATTTAGGACCTTAATTTCTCAGAACCTGAAACCATGCTAA 1404  
 Db 1334 TCTGTAGCCCAAGACATTTAGGACCTTAATTTCTCAGAACCTGAAACCATGCTAA 1389

RESULT 7  
 AEN60002  
 ID AEN60002 standard; cDNA; 1540 BP.  
 XX  
 AC AEN60002;  
 XX  
 DT 28-JUN-2002 (first entry)  
 XX  
 DE Novel human coding sequence SEQ ID NO: 413.  
 XX  
 KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;  
 KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;  
 KW neuroprotective; antiparkinsonian; protein therapy; EST;  
 XX expressed sequence tag; gene; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200222660-A2.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US26015.  
 XX  
 PR 11-SEP-2000; 2000US-0659671.  
 XX



(HYSE-) HYSEQ INC.

Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren P;  
Xue AJ, Yang Y, Wehrman T, Drmanac RT;WPI; 2002-292408/33.  
P-PSDB; ABB97589.An isolated polynucleotide for treating diseases associated with its  
encoded polypeptide such as cancer and multiple sclerosis -

Claim 1; SEQ ID NO 413; 509pp; English.

The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the invention.

Sequence 1540 BP; 477 A; 276 C; 324 G; 453 T; 0 other;

RY Match 57.5%; Score 808; DB 24; Length 1540;

t Local Similarity 100.0%; Pred. No. 5.8e-218;

ches 808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCTTGGAAATTGGATTGCTTCATCTTGTTTGGACATCAAGAGAAAGAGTT 60  
86 ATGCTTGGAAATTGGATTGCTTCATCTTGTTTGGACATCAAGAGAAAGAGTT 145  
61 TGTATGAAGGTTAGGGTGTTCAAAGATGTTTACCATGGACGAGCACTTCTCAACA 120  
146 TGTATGAAGGTTAGGGTGTTCAAAGATGTTTACCATGGACGAGCACTTCTCAACA 205  
121 GAGTGGTGGTTTACCTGGTCTCGAGAGAATAACACATCGTTCTGCTCTCACT 180  
206 GAGTGGTGGTTTACCTGGTCTCGAGAGAATAACACATCGTTCTGCTCTCACT 265  
181 ATACAAATCCCAATGCCATCAGAGATCAGTGGGTAAATCTTCAACTATCCAGGCC 240  
266 ATACAAATCCCAATGCCATCAGAGATCAGTGGGTAAATCTTCAACTATCCAGGCC 325  
241 TCATATTTGGAAACAGACAAAGATACCCGTTATCAATAGCTGGATGGAACAGATGGC 300  
326 TCATATTTGGAAACAGACAAAGATACCCGTTATCAATAGCTGGATGGAACAGATGGC 385  
301 AATGCGCAGAGACATGTGCAATGTTGCTACAGCTGGAAGATATAATGCTCAATAT 360  
386 AATGCGCAGAGACATGTGCAATGTTGCTACAGCTGGAAGATATAATGCTCAATAT 445  
361 TTAGATTGGATCAACGGTTTACGGGAATACATCCATGCTGTAAACAATCTCCGTTGTT 420  
446 TTAGATTGGATCAACGGTTTACGGGAATACATCCATGCTGTAAACAATCTCCGTTGTT 505  
421 GGTGCTGAGTGGCTTATTTATGATGTTCTCATGAAAAAATTTGAATATCCCTTCT 480  
506 GGTGCTGAGTGGCTTATTTATGATGTTCTCATGAAAAAATTTGAATATCCCTTCT 565  
481 AAAGTGCATCTGATTGGCCACAGCTGGGAGCACACCTGGCTGGGGAAGCTGGTCAAGG 540  
566 AAAGTGCATCTGATTGGCCACAGCTGGGAGCACACCTGGCTGGGGAAGCTGGTCAAGG 625  
541 ATACAGGCGCTTGGAGAATAACTGGTTGGACCAAGCTGGGCAATTTTCCACAACACT 600  
626 ATACAGGCGCTTGGAGAATAACTGGTTGGACCAAGCTGGGCAATTTTCCACAACACT 685  
601 CCNAAAGGAGTCAGGCTAGACCCCTCGGATGCCAATTTGTTGACGTTATTCATCAAAAT 660

Db 686 CCAAAGGAAGTCAGGCTAGACCCCTCGGATGCCAACTTGTGTGACGTTATTATCATCAAAAT 745  
QY 661 GCAGCTCGCATCTCTTTGAGCTTGGTGTGGAAACCATTTGATGCTTGTGGTCACTTGAC 720  
Db 746 GCAGCTCGCATCTCTTTGAGCTTGGTGTGGAAACCATTTGATGCTTGTGGTCACTTGAC 805  
QY 721 TTTTACCCAAATGGAGGAAGCACATGCCAGGATGTGAAGACTTTAATTACACCTTTACTG 780  
Db 806 TTTTACCCAAATGGAGGAAGCACATGCCAGGATGTGAAGACTTTAATTACACCTTTACTG 865  
QY 781 AAATTTAACTTCAATGCTTACAAAAAG 808  
Db 866 AAATTTAACTTCAATGCTTACAAAAAG 893

RESULT 8  
ABL69985  
ID ABL69985 standard; DNA; 1481 BP.  
XX ABL69985;  
AC ABL69985;  
XX  
DT 15-MAY-2002 (first entry)  
XX  
DE Pancreas cancer related gene sequence SEQ ID NO:8322.  
XX  
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
gene; ds.  
XX Homo sapiens.  
XX  
PN WO200194629-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-US10838.  
XX  
PR 05-JUN-2000; 2000US-209473P.  
PR 05-JUN-2000; 2000US-209531P.  
PR 18-SEP-2000; 2000US-233133P.  
PR 18-SEP-2000; 2000US-233617P.  
PR 20-SEP-2000; 2000US-234009P.  
PR 20-SEP-2000; 2000US-234034P.  
PR 20-SEP-2000; 2000US-234052P.  
PR 22-SEP-2000; 2000US-234509P.  
PR 22-SEP-2000; 2000US-234567P.  
PR 25-SEP-2000; 2000US-234923P.  
PR 25-SEP-2000; 2000US-234924P.  
PR 25-SEP-2000; 2000US-235077P.  
PR 25-SEP-2000; 2000US-235082P.  
PR 25-SEP-2000; 2000US-235134P.  
PR 25-SEP-2000; 2000US-235280P.  
PR 26-SEP-2000; 2000US-235637P.  
PR 26-SEP-2000; 2000US-235638P.  
PR 27-SEP-2000; 2000US-235711P.  
PR 27-SEP-2000; 2000US-235720P.  
PR 27-SEP-2000; 2000US-235840P.  
PR 27-SEP-2000; 2000US-235863P.  
PR 28-SEP-2000; 2000US-236028P.  
PR 28-SEP-2000; 2000US-236032P.  
PR 28-SEP-2000; 2000US-236033P.  
PR 28-SEP-2000; 2000US-236034P.  
PR 28-SEP-2000; 2000US-236109P.  
PR 28-SEP-2000; 2000US-236111P.  
PR 29-SEP-2000; 2000US-236842P.  
PR 29-SEP-2000; 2000US-236891P.  
PR 02-OCT-2000; 2000US-237172P.  
PR 02-OCT-2000; 2000US-237173P.  
PR 02-OCT-2000; 2000US-237278P.  
PR 02-OCT-2000; 2000US-237294P.  
PR 02-OCT-2000; 2000US-237295P.  
PR 02-OCT-2000; 2000US-237318P.

03-OCT-2000; 2000US-237425P.  
 03-OCT-2000; 2000US-237598P.  
 03-OCT-2000; 2000US-237604P.  
 03-OCT-2000; 2000US-237606P.  
 03-OCT-2000; 2000US-237608P.  
 01-NOV-2000; 2000US-244867P.  
 01-NOV-2000; 2000US-245084P.  
 (AVAL-) AVALON PHARM.  
 Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 Soppet DR, Weaver Z;  
 WPI; 2002-188264/24.  
 Screening for anti-neoplastic agent involves exposing cells to a  
 chemical agent to be tested for anti-neoplastic activity, and  
 determining a change in expression of a gene of a signature gene set -  
 Claim 1; SEQ ID 8322; 44pp; English.

The present invention describes a method (M1) for screening for an  
 anti-neoplastic agent. The method involves exposing cells to a chemical  
 agent to be tested for anti-neoplastic activity, determining a change in  
 expression of at least one gene (I) of a signature gene set, where (I)  
 comprises a sequence (S) selected from 8447 sequences (given in ABL6164  
 to ABL70110), or is at least 95% identical to (S), where a change in  
 expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 activity and can be used in gene therapy. M1 can be used for screening  
 an anti-neoplastic agent, and can be used for producing a product which  
 is the data collected with respect to the anti-neoplastic agent as a  
 result of M1, and the data is sufficient to convey the chemical  
 structure and/or properties of the agent. M1 can be used in the  
 treatment of cancer such as colon, breast, stomach, lung, thyroid,  
 esophageal, ovarian, kidney, prostate or pancreatic cancer,  
 adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
 infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
 carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 1481 BP; 399 A; 371 C; 379 G; 332 T; 0 other;

ary Match 27.5%; Score 386.2; DB 24; Length 1481;  
 at Local Similarity 57.1%; Pred. No. 1.2e-98;  
 tches 807; Conservative 0; Mismatches 588; Indels 18; Gaps 5;

1 ATGCTGGAATTCGATTGTGCTTCTTCTTGGACATCAGAGGAAAGAGTT 60  
 20 ATGCTGATCTCTGCAATCACAATTTCTCTGCTGGAGCAGCCAAAGAAAGAGTT 79  
 61 TGCTATGAAGAGTTAGGTTGTTTCAAGATGGTTTACCATGGACAGGACTTTCTCAACA 120  
 80 TGCTATGAGGACCTCGGTTGCTTTCTGACACTGAGCCCTGGGGCGGGACAGCAATCAGG 139  
 121 GAGTTGGTAGGTTTACCTGGTCTCCAGAGAGATAAAGTCTGTTCTGCTCTACACT 180  
 140 CCCTGAAATTCCTCCCTGGAGCCCTGGAAGATCGGCACCGCTTCTGCTGTACACC 199  
 181 ATACACATCCCAATGCTCATCAGGAGATCAGTGGGTTAATTCCTCAACTATCAAGCC 240  
 200 AATGAAACCCCAACAATTTCAATTTCTCTCTGATCCATCAACAATTGAGGCA 259  
 241 TCATATTTTGGAGACAGACATCACCCTGATCAACATAGTGG-----ATGGAAGAA 294  
 260 TCAATTTTCAATTTGAG 319  
 295 GATGGCAATGGCAGAGAGACATGCAATGTTGCTACAGCTGGAAGATATAAATGCG 354  
 320 GATGAGAGCTGGTGGACAGACATGTCGAAGAACTGTTGAGGTGAGGAGGTGAATGCG 379  
 355 ATTAATTTAGATTGGATCAACGGTTTCAAGGG-----AATACATCATCTGTAAACAATCTC 411  
 380 ATCTCGGTGGAGCTGGAAGAGAGGGTCTCCCAAGCCACCTACACACAGGCTGCCAACACG 439

QY 412 CGTCTTCTGCTGCTGAGTGGCTTATTTTATTGATGTTCTCATGAAAAAATTTGAATAT 471  
 DB 440 CGAGTGTGGCGGCCAGAGTGGCCAGATGCTCGACATCTTGTGACAGATATAGCTTAC 499  
 QY 472 TCCCTTTCTAAAGTGCATTTGATTTGGCCACAGCTTGGGAGACACCTGGCTGGGAAGCT 531  
 DB 500 CCCCCTTCCAAAGTTTCACTCTCATTTGGCCACAGCTTGGGAGCCACGCTGGCTGGAGAGCA 559  
 QY 532 GGGTCAAGGATACAGGCTTGGAGCAATAAATGCTGGTGGACCCAGCTGGGCCATTTTTC 591  
 DB 560 GGAAGCAGACTCGAGCCCTGACAGAGATTAAGGTTTGGATCTCTGTAGAACAGATTTC 619  
 QY 592 CACAACACTCCAAAGGAAGTCAAGCTAGACCCCTCGGATGCCAACCTTTTGTGACGTTAT 651  
 DB 620 GAGAGTACTCTCGAAGAGGTGCGACTTGTATCCCTGTGATGCTGACTTTGTTGATGTGAT 679  
 QY 652 CATACAAATCCAGCTCGCATCTCTTTGAGCTTGGTGGAAACCATTTGATGCTTGTGGT 711  
 DB 680 CACAGGATCAGCTCCCTGATCCCATTTCTTGGGTTTGGAAACGAAACCAACAGATGGGT 739  
 QY 712 CATCTTGACTTTTACCCAAATGGAGGGAAGACATGCCAGGATGTGAAGACTTAATTACA 771  
 DB 740 CATCTTGACTTTCTCCCAATGGAGGAGAGAGATGCCGGATGCAAGAA---GAATGCC 796  
 QY 772 CCTTTACTGAAATTTAACTTCAATGCTTACAAAAAGAAATGGCTTCTCTTTGACTGT 831  
 DB 797 CTGCTCAGATCTGATCTAGATGGCATCTGGGCGGGAACCCGGGACTTTGTGGCTTGC 856  
 QY 832 AACCATGCCCGAAGTTATCAATTTATGCTGAAAGCATTTCTTAATCTCTGATGCTTATT 891  
 DB 857 AATCACCCTAAGAGCTTCAAGTATTAATTTGGAAGCATCTCAATCCCGATGGGTTTGTCT 916  
 QY 892 GCTTATCTTTGATGCTTACACATCTTTTAAAGCAGGAATGCTTCTTTTGTTCCTTCAAA 951  
 DB 917 GCATATCCCTGCACTTCTTACAGTCTCTTTGAGTGTGACAGTCTTCCCGTGTCCAGAT 976  
 QY 952 GAAGGTTGGCCCAACAATGGTCTATTTGCTGATAGATTTTCACTTCAAAAAATATGAAGCT 1011  
 DB 977 CAAGGATGCCAGATGGTCTATGCTGATTAATTTGCTGGCAGGACAGATGA---A 1033  
 QY 1012 AATGGATCACTTATTTTAAACACAGGCTCCCTTTCCCATTTTGGCGGTGGAGGCAC 1071  
 DB 1034 GAGCAGCAGAAATTTCTTTGAACACAGGAGAGGCTAGCAATTTGCTCGCTGGAGATAT 1093  
 QY 1072 AATTTCTGTTAACTCAGTGGAGCGAGTCACTCAAGGAATGCTTCTTCTTCTGCTA 1131  
 DB 1094 GGGGTTTCCATCACACTGTCTGAAAGAACAGCCACT---GGTCAAGTCAAAAGTTGCTTTG 1150  
 QY 1132 GCGGGGCAATTTGGGAAAACTGGGAGTTTGGCATTGTGAGTGGAAAACTTTGAGCCAGGC 1191  
 DB 1151 TTTGGAATAAGGGAACACTCACAGTACAGCATCTTTCAGGGGATTTCTCAAACCCAGGC 1210  
 QY 1192 ATGACTTACAAAAATTAATCGATCGAGATGTTACGTTGGAACATTTACAGTGTTCAG 1251  
 DB 1211 TCAACCATTTCTATGAGTTTGTATGCAAGCTGGATGTTGGAACAATTTGAAAAAGTCAAG 1270  
 QY 1252 TTCACTCGAAAAAACAATTTGTAAGATTTCTAGAATAAGTTGGGAGCAGAAATGGTG 1311  
 DB 1271 TTTCTTTGGATTAACAATGATTAATCCACCCCTCCCAAGTGGGTGCCACCAAGATC 1330  
 QY 1312 ATAAATACATCTGGGAAATATGGATATAAATCTCTCTGTAGCCAAAGACATTTATGGGA 1371  
 DB 1331 ACTGTGCAAAAGGGAAG 1390  
 QY 1372 CCTAATTTTCTCAGAACCTGAAACCATGCTAA 1404  
 DB 1391 GAAGACACGCTGCTACCCCTCAGCCCTGCTTAA 1423

RESULT 9  
 AAS81082  
 ID AAS81082 standard; cDNA; 1427 BP.  
 XX

AA591082;

13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #16886.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US09831.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Dzmanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

P-PSDB; AEG16895.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 1; SEQ ID No 16886; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AA564197-AA594564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 1427 BP; 389 A; 354 C; 362 G; 322 T; 0 other;

xy Match 25.2%; Score 353.8; DB 23; Length 1427;  
t Local Similarity 57.0%; Pred. No. 1.8e-89;  
ches 808; Conservative 0; Mismatches 587; Indels 22; Gaps 8;

1 ATGCTTGGAAATTTGGATTGTCATCTTTGTTTGGACATCAAGAGGAAAGAGTT 60

20 ATGCTGATCTTGGACATCACTTTTCTGCTGGGAGCAGCCAAAGGAAAGAGTT 79

61 TGTATGAGAGGTTAGGGTTTCAAGATGGTTTACCATGGACGACACTTCTCAACA 120

80 TGTATGAGACCTCGGGTGCTTTCTGACATGAGCCCTGGGGCGGACAGCAATCAGG 139

121 GAGTTGGTAGGTTTACCTGGTCTCCAGAGAGATAAACACTCGGTTCTCTCTCACT 180

140 CCCTGAAATCTCCCTTGGAGCCCTGGAAGATCGGACCCCGCTTCTGCTACACC 199

QY	181	ATACACAATCCCAATGCTTATCAGGAGATCAGTGGGTTAATTTCTTCAACTATCCAGCC	240
Db	200	AATGAACACCAACAACATTTCAAAATTTCTCTCTCTGATCCATCAACAAATTTGAGGCA	259
QY	241	TCATATTTTGGAAACAGACAGATCACCGTATCAACATAGCTGG-----ATGAAACA	294
Db	260	TCAAATTTTCAATGGACAGAAAGACCGGTTTCATCATCCATGGCTTCATAGACAAAGGA	319
QY	295	GATGCAAAATGGCAGAGAGACATGTGCAATGTGTTGTACAGCTGGAGATATAAATGC	354
Db	320	GATGAGAGCTGGGTGACAGACATGTGCAAGAACTGTTTCGAGGTGGAGGTTGAATGC	379
QY	355	AT-TAATTTAGATTGGATCAACGGTTTCAAGGAA---TACATCCATGCTTAACAATCT	410
Db	380	ATCTTCTGTTGGACTGGAAGAGGGCTCCCAAGCCACCTTACACAGGCTGCCAACAAGT	439
QY	411	CGGTGTTGTTGCTGAGTGGCTTATTTTATTTGATGTTCTCATGAAAAAATTTGAATA	470
Db	440	GGAGTGGTGGGCGCCAGGTGGCCAGATGCTCGACATCTCTTGACAGAGTATAGCTA	499
QY	471	TTCCCTTCTAAAGTGCACCTTGAATGGCCACAGCTTGGAGCACACCTGGCTGGGAGC	530
Db	500	CCCCCTTCCAAAGTTCACTTCATTTGGCCACAGCTGGAGCCCACTGGCTGGAGGCG	559
QY	531	TGGTCAAGGATACCAAGCCTTGG--AAGATAACTGGTGGACCCAGCTGGGCCAATTT	588
Db	560	AGGAAGCAAGACTCCAGGCTTGGCAAGGATTACAAGGTTGGATCTCTGTAAGACAAAT	619
QY	589	TTCCCAACACTCCAAAGGAAGTACGG--TAGACCCCTCGGATGCCAACTTTGTTGACGT	647
Db	620	TTGAGAGTACTCTGGAAGAGTGGGACTTTGATCCCTCTGATGCTGACTTTGTTGATG	679
QY	648	TATTCATAAATGCAATGCTGCTCTCTTTTGAAGCTTGGTGGTGGAAACCAATGATGTTG	707
Db	680	GATTCACAGGATGAGCTCCCTGATCCCTTCTTGGGTTTGGAAACCAACAGAT	739
QY	708	TGGTCACTTGGATTTTACCAATGGAGGGAAGCAGATGCCAGGATGTGAGACTTAAT	767
Db	740	GGGTCACTTGGATTTTCCCAATGGAGGAGAGATGCCGGGATGCAAGAAAG---AA	796
QY	768	TACACCTTTTACTGAAATTTAACTTCAATGCTTACAAAAAGAAATGGCTTCTTCTTGA	827
Db	797	TGCCCTGCTCAGATCGTGGATCTAGATGGCATCTGGGCGGAACCCGGGACTTTGGGC	856
QY	828	CTGTAAACATGCCGGAAGTTATCAATTTATGCTGAAAGCATCTTAACTCTGATGCAAT	887
Db	857	TTGCAATCACCTAAGAGCTACAAGTATTACTTGGAAAGCATCTCAATCCCGATGGGTT	916
QY	888	TATTCCTTATCTTGTAGATCCTACATCTTTTAAAGCAGGAAATGCTTCTTTCTTC	947
Db	917	TGCTGCATATCTCTGCACTTCTTCAAGTCTTTGAGTCTGACAGTGTCTCCGTTGCC	976
QY	948	CAAGAGAGTTGCCCAACAATGGTTCATTTTGTGATAGATTTCATTTCAAAAAATATGAA	1007
Db	977	AGATCAAGGATGCCACAGATGGTCTACTATGCTATAAATTTGCTGGCAGGACAAGTGA	1036
QY	1008	GACTAATGGATCACAATTTTAAACACAGGAGTCTTCCCAATTTGGCGTTGGAG	1067
Db	1037	---AGAGCAGCAGAAATTTCTTCTTGAACACAGGAGAGGTAGCAATTTGCTCGTGGAG	1093
QY	1068	GCACAAATTTGCTGTTAACTCAGTGGAGCGAAGTCACTCAAGGAACCTGCTTTCTTCG	1127
Db	1094	ATATGGGTTTCCATCAGCTCTGCTGGAAGACAGCCACT--GGTCAGATCAAGTTGC	1150
QY	1128	TGTAGCGGGCAATTTGGAAACTGGGGAGTTTGCATTTGCTAGTGGAAAACTTGAGCC	1187
Db	1151	TTTGTGTTGAAATAAGGGAAACACTCACAGTACAGATCTTTCAGGGGGATTCTCAACC	1210
QY	1188	AGGCATGACTTTACACAAATTTAATCGATGAGATGTTAAGCTTGGAAACATTAAGTGT	1247
Db	1211	AGGCTCAACCCATCTCTATGATGTTTGAATGCAAGCTGGATGTTGGAAACAATTGAGAAAT	1270

1248 TCAGTTCATCTGGAAAAACATTTGTTTGAAGATTCTCAGATAAGTTGGAGCAGAAAT 1307  
 1271 CAAGTTTCTTTGGATAACAATGATGATAAATCCAACTCCCAAGTGGTGGCCAA 1330  
 1308 GGTGATAATACATCTGGAAATATGGATATAAATCTACCTTCTGTAGCCAAAGCATTTAT 1367  
 1331 GATCACTGTGCAAGAGGAGAGAGACACAGTGTACAACTTCTGTAGCAGACACAGT 1390  
 1368 GGGACCTAATATTCTCCAGAACCTTGAAACCATGCTAA 1404  
 1391 GCGGAGACACAGCTGCTCACCTTCAGCCCTGCTAA 1427

LT 10

9552

ABL59552 standard; cDNA; 1454 BP.

ABL59552;

16-JUL-2002 (first entry)

Human triacylglycerol lipase cDNA SEQ ID NO:52.

Human; triacylglycerol lipase; enzyme; tumour; lipid associated gene;  
 lipid metabolism; lipid synthesis; gene; ss.

Homo sapiens.

WO200227028-A1.

04-APR-2002.

27-SEP-2001; 2001WO-US030366.

28-SEP-2000; 2000US-0676052.

(ATAI-) ATAIRGIN TECHNOLOGIES INC.

Skinner MK, Patton JL, Chaudhary J;

WPI; 2002-402054/43.

Identifying tumor characteristics in a tissue sample taken from a patient, involves determining the copy number or expression level of genes associated with lipid metabolism, synthesis or action -

Example 1; Page 109-110; 113pp; English.

The present invention describes a method for identifying tumour characteristics, comprising measuring a copy number or expression level of at least two genes associated with lipid metabolism, synthesis, or action in cells from a patient tissue sample, and comparing the results with a copy number or expression level of the genes in a normal cell. Also described is an array of nucleic acid polymers immobilised on a solid support, comprising a solid support, at least two different nucleic acid polymers which are each specific for a different gene associated with lipid metabolism, synthesis or action, where each nucleic acid polymer is located at a predetermined position on the solid support, and the array comprises nucleic acid polymers which are specific for less than 100 genes other than the selected genes. The method is useful for determining tumour characteristics in a tissue sample taken from a patient. The present sequence represents a human lipid-associated gene related cDNA sequence, which is used in the exemplification of the present invention.

Sequence 1454 BP; 415 A; 313 C; 349 G; 377 T; 0 other;

ery Match 24.4%; Score 342.6; DB 24; Length 1454;  
 st Local Similarity 57.0%; Pred. No. 2.6e-86;  
 tches 791; Conservative 0; Mismatches 569; Indels 27; Gaps 8;

29 TGTCTTTGGCACATCAAGAGCAAGAGTTTCTATGAAGTTAGGTGTTTCAAG 88

Db 26 TGCTGTGGGAGCAGTAGCAGGAAAAAGAGTTTGTCTACGAAAGACTCGGCTGCTTCAGTG 85  
 QY 89 ATGCTTTTACCATGGACGAGACTTTTCTACACAGAGTTGGTAGGTTTACCTGGTCTCCAG 148  
 Db 86 ATGACTCCCATGTCAGGAATTCGGAAGAGCCCTCCATATATTGGCTTGGTCTCCAA 145  
 QY 149 AGAAGATAAACACTCGTTTCTGCTCTACACTATACAAATCCCAATGCTTATCAGGAGA 208  
 Db 146 AAGATGCAACACCCGCTTCTCTATATATACTAATAGAAACCCAAACAATTTCAAGAAG 205  
 QY 209 TCAGTGGGTTAATTTCTTCAACTATCCAGCCCTATATTTTGGACAGACAAGATCACCC 268  
 Db 206 T---TGCCGAGATTTCATCAAGCATCAGTGGCTCCAAATTTCAAAAACAAATAGAAAACATC 262  
 QY 269 GTATCAACATAGCTGGAT-----GGAACACAGATGGCAATGGCAGAGACATGTGCA 322  
 Db 263 GCITTTATTATTGATTCATAGACAGGGAGAGAAACCTGGCTGGCCATGTGTGCA 322  
 QY 323 ATGTGTTGCTACAGCTGGAAGATATAAATTGCAATTAATTTAGATTGGATCAACGGTTAC 382  
 Db 323 AGAATCTGTTCAAGGTGGAAGTGTGAACCTGTATCTGTGAGACTGGAAGGTGGCTCCC 382  
 QY 383 GG---GAATACATCCATGCTGTAAACAATCTCGTCTGTTGCTGTGAGGTGGCTTATT 439  
 Db 383 GAATGATACACACAGCTCCAGACATCAGGATCTGTGGAGCAGAGTGGCATATT 442  
 QY 440 TTATTGATTTCTCATAAAAAATTTGAAATTTTCCCTTTCTAAAGTGCACTTGTATGGCC 499  
 Db 443 TTGTTGAATTTCTCAGTGGCGTTCGGTTACTCACTTCCAACTGTCATGTCAITGGCC 502  
 QY 500 ACAGCTTGGGAGCACACCTGGCTGGGAGAGCTGGGTCAAGGATACCAGG---CCTTGGAA 556  
 Db 503 ACAGCTTGGGTGCCACGCTGCTGGGAGGCTGGAGAGAGAACCAATGGGACCATTTGGAC 562  
 QY 557 GAATAACTGGGTTGGACCCAGCTGGGCCATTTTTCACAAACACTCCAAAGGAAGTCAGGC 616  
 Db 563 GCATCACAGGTTGGACCCAGCAGAACCTTGTCTTCAGGGCACACCTGAATTAGTCCGAT 622  
 QY 617 TAGACCTCGGATGCGAATTTGTTGAGCTTATTATCATAAAATGAGCTCGCATCTCT 676  
 Db 623 TGGACCCCGCAGTATGCCAAATTTGTGGATGTAATTCACACGGATGGTGGCCCCCATAGTCC 682  
 QY 677 TTGAGCTTGGTTGGAACCATTTGATGCTTGTGGTTCATCTTGACTTTTACCCAAATGGAG 736  
 Db 683 CCAATTTGGGTTTGGAAATGAGCCAACTGCTGGGCCACCTAGATTCTTCCAAATGGAG 742  
 QY 737 GGAAGCACATGCCAGGATGGAAGACTTAATTACACCTTTTACTGAAATTTAACTTCAATG 796  
 Db 743 GAGTGGAAATGCTGGATGTAAAAAGAACATT---CTCTCTCAGATTGTGGACATAGACG 799  
 QY 797 CTTACAAAAAAGAAATGGCTTCTCTTCTGACTGTAAACCATGCCGAAAGTTATCAATTTT 856  
 Db 800 GAATCTGGGAAGGACTCGAGACTTTGGCGCTGTAAATCACTTAAGAAGCTACAAATATT 859  
 QY 857 ATGCTGAAGCATTTTAATCTCTGATGCAATTTATTGCTTATCTCTTGTAGATCCATACAT 916  
 Db 860 ACATGATAGACTCGTCAACCCCTGATGGCTTTGCTGGATTCCCTGTGCTCTTACAAAG 919  
 QY 917 CTTTAAAGCAGAAATTTGCTTTTGTTCCAAAGAGTTGCCCAACATGGGTGCTATT 976  
 Db 920 TCTTCACTGCAACAAAGTGTTTCCCTTGTCCAAGTGGAGCTGGCCACAGATGGGTCACT 979  
 QY 977 TTGCTGATGATTTCACTTCAAAAATATGAAGACTAATGAATGATCATTATTTTAAACA 1036  
 Db 980 ATGCTGATGATATCTCTGGGAAA---ACAAATGATGTGGGCCAGAAATTTTATCTAGACA 1036  
 QY 1037 CAGGTCCTTTTCCCATTTGCCGTTGGAGCACAATTTGCTGTAACTCAGTGGNA 1096  
 Db 1037 CTGGTATGCCAGTAATTTTGACGCTTGGAGTATAAGGTATCTGTGCACACTGTCTGGAA 1096  
 QY 1097 GCGAAGTCACTCAAGAACTGTCTTTTCTTGTAGGGGGGCAATTTGGAAAACTGGGG 1156  
 Db 1097 AAAAGGTAC---AGACACATACATAGTTTCTTTTGTTCGAAATTAAGGAACTCTAAGC 1153

1157 AGTTTGCCATTGTCAGTGGAAACCTTGAGCCAGGCATGACCTTACACAAAATTATCGATG 1216  
 |||||  
 1154 AGTATGAAATTTTCAAGGGCACTCTCAACCCAGATAGTACTCATTCCTCAATGAATTTGACT 1213  
 |||||  
 1217 CAGATGTTAACTGTTGGAACATTACAAGTGTTCAGTTCATCTCGAATAAACATTTGTTG 1276  
 |||||  
 1214 CAGATGTGGATGTTGGGACCTTGCAGATGGTTAAATTTATTTGGTATAACAATGTGATCA 1273  
 |||||  
 1277 AAGATTCTCAGAAATAAGTTGGGAGCAGAAATGGTGATATAATACATCTGGGAATATGGAT 1336  
 |||||  
 1274 ACCCACTTTACTAGATGGAGGATCCAGATTATAGTGGAGAC---AAATGTTGGAA 1330  
 |||||  
 1337 ATAAATCTACCTTCTGTAGCCAGACATATATGGACCTTAATTTCTCCAGAACCTGAAAC 1396  
 |||||  
 1331 AACAGTTCAACTTCTGTAGTCCAGAAACCGTCAGGAGGAAGTTCTGTCTACCTCACCAC 1390  
 |||||  
 1397 CATGCTA 1403  
 |||||  
 1391 CQTGTTA 1397  
 |||||

r 11

205

ABK44205 standard; cDNA; 1471 BP.

ABK44205;

21-MAY-2002 (first entry)

cDNA #145 encoding human pancreatic tumour protein #2.

human; pancreatic tumour protein; immune response; pancreatic cancer;  
 development of cancer; cancer progression; cytostatic; gene; ss.

Homo sapiens.

NO200212331-A2.

14-FEB-2002.

36-AUG-2001; 2001WO-US24619.

37-AUG-2000; 2000US-223130P.

30-JAN-2001; 2001US-265447P.

15-MAY-2001; 2001US-291201P.

(CORI-) CORIXA CORP.

Pyle RA, Xu J, Kalos MD;

MPI; 2002-241741/29.

P-PSDB; AAU87690.

Novel polynucleotide encoding pancreatic tumour polypeptides, useful in  
 pharmaceutical compositions, e.g. vaccines, for treating pancreatic  
 cancers -

Claim 1; Page 157; 167pp; English.

The present invention relates to the isolation of cDNA sequences  
 encoding human pancreatic tumour proteins. The polynucleotide  
 sequences encoding human pancreatic tumour proteins are useful for  
 stimulating an immune response in a patient and treating pancreatic  
 cancer in a patient. A host cell that expresses these polynucleotides  
 is useful for determining the presence of cancer in a patient. A  
 composition comprising the polynucleotide, its encoded protein, or an  
 antibody that binds to the protein may be used in the diagnosis,  
 prevention and/or treatment of diseases, particularly pancreatic  
 cancer. The sequences of the invention are also useful in pharmaceutical  
 compositions, e.g. vaccines, for the diagnosis and treatment of  
 pancreatic cancer. Such compositions may be useful for inhibiting the  
 development of cancer in a patient, or as markers for the progression

CC of cancer. The polynucleotide sequences may also be used as probes  
 CC or primers for nucleic acid hybridisation assays. ABK44061-ABK44209  
 CC represent cDNA sequences encoding for human pancreatic tumour proteins.

XX Sequence 1471 BP; 423 A; 317 C; 353 G; 378 T; 0 other;

Query Match 24.4%; Score 342.6; DB 24; Length 1471;  
 Best Local Similarity 57.0%; Pred. No. 2.6e-86;  
 Matches 791; Conservative 0; Mismatches 569; Indels 27; Gaps 8;

QY 29 TGTTCTTTGGCAGATCAAGAGGAAAGAGTTTCTATGAAGTTAGGGTGTTCAAAG 88  
 |||||  
 Db 38 TGCTGCTGGGAGCTAGCAGGAAAGAGTTTGTACGAAAGACGCGCTGCTTCAGTG 97  
 |||||  
 QY 89 ATGTTTACCATGACACAGGAGACTTCTCAACAGAGTTGGTAGTTTACCCCTGGTCTCCAG 148  
 |||||  
 Db 98 ATGACTCCCATGCTCAGGAATTACGGAAAGACCCCTCCATATATTGCTTGGTCTCCAA 157  
 |||||  
 QY 149 AGAGATTAACACTCGTTTCTGCTCTACACTATACAAATCCAAATGCCATGCCATCAGGAGA 208  
 |||||  
 Db 158 AAGATGTCAACACCCCGCTTCTCTCTATATATACTAATGAGAACCCCAACAACTTTCAAGAAG 217  
 |||||  
 QY 209 TCAGTGGCGTTAATTCTTCAACTATCCAGCCTCATATTTTGGAAACAGACAAGATCACCC 268  
 |||||  
 Db 218 T---TGCCGCGAGATTCAATCAGCATCAGTGGCTCCATTTCAAAAACAATAGAAAACCTC 274  
 |||||  
 QY 269 GTATCAACATAGCTGGAT-----GGAAAAACAGATGGCAATGGCAGAGAGACATGTGCA 322  
 |||||  
 Db 275 GCTTTATTATTCTAGTATTATAGACAAAGGAGAGAAAGAACTGGCTGGCCAAATGTGTGCA 334  
 |||||  
 QY 323 ATGTGTTGCTACAGCTGGAAGATATAAATTGCAATTAATTAGATTGSAATCAACGGTTTCA 382  
 |||||  
 Db 335 AGAATCTGTTCAAGTGGAAAGTGTGAATCTGTTGTTGGACTGGAAGGTGGCTGCC 394  
 |||||  
 QY 383 GG---GAATACATCCATGCTGTAAACAATCTCCGTGTTGTTGCTGAGGTGGCTTAAT 439  
 |||||  
 Db 395 GAATGGGATACACACAAGCCTCGCAGAAACATCAGGATCGTGGGAGCAGAAAGTGGCATATT 454  
 |||||  
 QY 440 TTATTGATGTTCTCATGAAAAAATTTGAATATTTCCCTTCTAAAGTGCACCTTGATTGGCC 499  
 |||||  
 Db 455 TTGTGAAATTTCTTCAGTCCGCGTTGGTTTACTCACCTTCCAAACGTGTCATGTCATTGGCC 514  
 |||||  
 QY 500 ACAGCTTTGGGAGCACACCTGGCTGGGGAAGCTGGGTCAAGGATACCAGG---CCTTGGAA 556  
 |||||  
 Db 515 ACAGCCTGGGTGCCACCGCTGCTGGGAGGCTGGAAGGAGAACCAATGGGACCATTTGGAC 574  
 |||||  
 QY 557 GAATAACTGGGTTGGACCCAGCTGGGCCATTTTTCACAACTCCCAAGAGGAGTCAGGC 616  
 |||||  
 Db 575 GCATCACAGGGTTGGACCCAGCAGAACCTTGTCTTCAGGGGCACACCTGAATTAGTCCGAT 634  
 |||||  
 QY 617 TAGACCCCTCGGATGCCAACCTTTGTTGACGTTTATTCATAAAATGCAGCTCGCATCCTCT 676  
 |||||  
 Db 635 TGGACCCCGAGGATGCCAAATTTGTGGATGTAATTCACCGATGTGGTGGCCCATAGTCC 694  
 |||||  
 QY 677 TTGAGCTGTTGTTGGAAACCATTCATGCTGTTGCTGCTGCTGCTTTTACCCAAATGGAG 736  
 |||||  
 Db 695 CCAATTTGGGTTTGGAAATGAGCCAAAGTCGTGGGCCACCTAGATTTCTTTCCAAATGGAG 754  
 |||||  
 QY 737 GGAAGCATGCCAGGATGTGAAGACTTAATTACACTTTTACTGAAATTTAATCTCAATG 796  
 |||||  
 Db 755 GAGTGGAAATGCTCGGATGTAAAGAAAGAACAT---CTCTCTCAGATTGGACATAGACG 811  
 |||||  
 QY 797 CTTACAAAAAAGAAATGGCTTCCTTTGACTGTAAACCATGCCGAAGTTATCAATTTT 856  
 |||||  
 Db 812 GAATCTGGAGGGGACTCGAGACTTTTGGCGSCCTGTAATCACTTAAAGAGCTACAAATATT 871  
 |||||  
 QY 857 ATGCTGAAGCAATCTTAATCTCGATGATTAATTCCTTATCTCTGCTAGATCTACACAT 916  
 |||||  
 Db 872 AACTGTAGATGCTCAACCCCTGATGGCTTTGCTGGATTCCCTGCTCTTCAACG 931  
 |||||  
 QY 917 CTTTAAAGCAGGAAATTTGCTTTTGTTCAAAAAGAGGTTCGCCCAACAATGGGTCAAT 976  
 |||||  
 Db 932 TCATTCACTGCAACAGTGTTCCTTGTCCCAAGTGGAGGCTGCCCCACAGATGGGTCACT 991  
 |||||

977 TTGCTGATAGATTTCACATCTCAAAATATGAAGACTAATGGATCACATTAATTTTAAACA 1036  
992 ATGCTGATAGATATCTCTGGGAAA---ACAAATGATGTGGCCAGAAATTTTATCTAGACA 1048  
1037 CAGGCTCCCTTTCCCAATTTGCCGTTGGAGGCACAAATTTGTTAACTCAGTGGAA 1096  
1049 CTGATGATGACCAATTAATTTTCACGTTGGAGGTATAAGGTATCTGTCACTGTCTGGAA 1108  
1097 GCGAAGTCACTCAAGGAACCTCTCTTTCTGTGTAGCGGGGCAATTTGGGAAACTGGGG 1156  
1109 AAAAGGTTAC---AGGACACATACTAGTTCTTTCTGCGGAATAAAGGAACCTTAAGC 1165  
1157 AGTTGCCAATGTAGTGGGAACTTGAGCAGGCATGCTTACACAAATTAATGCGATG 1216  
1166 AGTATGAATTTTCAAGGGCACTCTCAACACAGATAGTACTATTCCAATGAATTTGACT 1225  
1217 CAGATGTTTAAAGTTGGGAAACATTACAAAGTGTCTAGTTTCATCTCGGAAACATTTGTTG 1276  
1226 CAGATGTGATGTTGGGACTTGCAGATGGTTAAATTTATTTGGTATAACATGTGATCA 1285  
1277 AAGATTTCAAGAAATAGTTGGGACAGAAATGGTGATAAATACATCTGGGAAATATGGAT 1336  
1286 ACCCAACTTTACCTAGATGGGAGCATCCAAGATTATAGTGGAGAC---AAATGTTGGAA 1342  
1337 ATAAATCTACCTTCTGTAGCCAGACATTAATGGACCTAATATTTCTCAGAACCTGAAC 1396  
1343 AACAGTTCAACTTCTGTAGTCCAGAAACCTCAGGGAGGAAGTTCTGCACCTCACAC 1402  
1397 CATGCTA 1403  
1403 CGTGTTA 1409

LT 12

9968

ABL69968 standard; DNA; 1471 BP.

ABL69968;

15-MAY-2002 (first entry)

Pancreas cancer related gene sequence SEQ ID NO:8305.

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
gene; ds.

Homo sapiens.

WO200194629-A2.

13-DEC-2001.

30-MAY-2001; 2001WO-US10838.

05-JUN-2000; 2000US-209473P.

05-JUN-2000; 2000US-209531P.

18-SEP-2000; 2000US-233133P.

18-SEP-2000; 2000US-233617P.

20-SEP-2000; 2000US-234009P.

20-SEP-2000; 2000US-234034P.

22-SEP-2000; 2000US-234052P.

22-SEP-2000; 2000US-234509P.

25-SEP-2000; 2000US-234567P.

25-SEP-2000; 2000US-234923P.

25-SEP-2000; 2000US-234924P.

25-SEP-2000; 2000US-235077P.

25-SEP-2000; 2000US-235082P.

26-SEP-2000; 2000US-235638P.  
27-SEP-2000; 2000US-235711P.  
27-SEP-2000; 2000US-235720P.  
27-SEP-2000; 2000US-235840P.  
27-SEP-2000; 2000US-235863P.  
28-SEP-2000; 2000US-236028P.  
28-SEP-2000; 2000US-236032P.  
28-SEP-2000; 2000US-236033P.  
28-SEP-2000; 2000US-236034P.  
28-SEP-2000; 2000US-236109P.  
28-SEP-2000; 2000US-236111P.  
28-SEP-2000; 2000US-236842P.  
29-SEP-2000; 2000US-236891P.  
02-OCT-2000; 2000US-237172P.  
02-OCT-2000; 2000US-237173P.  
02-OCT-2000; 2000US-237278P.  
02-OCT-2000; 2000US-237294P.  
02-OCT-2000; 2000US-237295P.  
02-OCT-2000; 2000US-237316P.  
03-OCT-2000; 2000US-237425P.  
03-OCT-2000; 2000US-237598P.  
03-OCT-2000; 2000US-237604P.  
03-OCT-2000; 2000US-237606P.  
01-NOV-2000; 2000US-244867P.  
01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

Soppet DR, Weaver Z;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a  
chemical agent to be tested for anti-neoplastic activity, and  
determining a change in expression of a gene of a signature gene set -

Claim 1; SEQ ID 8305; 44pp; English.

The present invention describes a method (M1) for screening for an  
anti-neoplastic agent. The method involves exposing cells to a chemical  
agent to be tested for anti-neoplastic activity, determining a change in  
expression of at least one gene (I) of a signature gene set, where (I)  
comprises a sequence (S) selected from 8447 sequences (given in ABU61664  
to ABU70110), or is at least 95% identical to (S), where a change in  
expression is indicative of anti-neoplastic activity. (I) has cytostatic  
activity and can be used in gene therapy. M1 can be used for screening  
an anti-neoplastic agent, and can be used for producing a product which  
is the data collected with respect to the anti-neoplastic agent as a  
result of M1, and the data is sufficient to convey the chemical  
structure and/or properties of the agent. M1 can be used in the  
treatment of cancer such as colon, breast, stomach, lung, thyroid,  
oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
carcinoma, papillary carcinoma and Wilm's tumour.

Sequence 1471 BP; 423 A; 317 C; 353 G; 378 T; 0 other;

Query Match 24.4%; Score 342.6; DB 24; Length 1471;

Best Local Similarity 57.0%; Pred. No. 2.6e-86;

Matches 791; Conservative 0; Mismatches 569; Indels 27; Gaps 8;

Qy 29 TGTTCCTTGGCCACATCAAGAGGAAAGAGTTTGTCTATGAAAGGTTAGGGTGTTCAAAG 88

Db 38 TGCTGCTGGAGCAGTAGCAGGAAAGAGTTTGTCTACGAAAGCTCGGCTGCTCAGTG 97

Qy 89 ATGCTTACATGACGACAGGACTTCTCAACAGAGTTGGTAGGTTTACCTGGTCTCCAG 148

Db 98 ATGACTCCCATGGTCAGGAATACGGAAGACCCCTCCATATATGCTGCTGCTCAA 157

Qy 149 AGAAGATAAACACTCGTTCTCTGCTCTACACTATACACAATCCCAATCCCTATCAGGAGA 208

158 AAGATGTCACACCGCTTCTCTCTATATCTAATAGAGAACCCAAACAACTTCAAGAAG 217  
 209 TCAGTGGGGTAAATCTTCAACATATCAAGCCTCATATTTTGGACAGACAGATCACCC 268  
 218 T---TGCGCGAGATTCATCAAGCATCAGTGGCTCCATTTTCAAAACAATAGAAAATC 274  
 269 GTATCAACATAGTGGAT-----GGAACACAGATGGCAAAATGGCAGAGACATGTGCA 322  
 275 GCTTTATATTCATGATTCATAGACCAAGGAGAGAAAACCTGGCTGGCCAATGTGTGCA 334  
 323 ATGTGTGTACAGCTGGAGATATTAATTTAGATTTAGATTTAGATTTAGATTTAGATTT 382  
 335 AGAATCTGTTCAAGGTGGAAAGTGTGAACATGATCTGTGTGGACTGGAAAGTGGCTCCC 394  
 383 GG---GAATACATTCATGCTGTAAACAAATCTCGTGTGTGTGTGTGTGTGTGTGTGT 439  
 395 GAATCGATACACACAGCCTCGCAGACATCAGGATCGTGGGAGCAGAGTGGCATATT 454  
 440 TTATTTGATTTCTCATGAAMAAATTTGAATATTTCCCTTCTTAAAGTGCACTTGATGGCC 499  
 455 TTGTGTAATTTCTTCAGTGGGCTTGGTTCAGTCTACCTTCCAACTGTCATGTCATGGCC 514  
 500 ACAGCTTTGGGAGCACACCTGGCTGGGAGAGCTGGGTCAAGGATACACAG---CCTTGGAA 556  
 515 ACAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 574  
 557 GAATACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 616  
 575 GCATCAAGGTTGGACCCAGCAGACACCTTGGCTTTCAGGGCAGACCTGAATAGTCCGAT 634  
 617 TAGACCCCTCGGATGCCAATTTTGTGTGGTGTATTCATCAACAAATGCAGCTGCCCTCT 676  
 635 TGACCCCGACGATGCCAATTTTGTGTGGTGTATTCATCAACAAATGCAGCTGCCCTCT 694  
 677 TTGAGCTGTGTGTGAACCAATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 736  
 695 CCAATTTGGGTTTGAATGAGCAAGTGGTGGGCACTAGATTTCTTCCAATGGAG 754  
 737 GGAAGACATGCCAGATGGAAGCTTAAATACACCTTTACTGAAATTAACCTCAATG 796  
 755 GAGTGAATGCTGTGATGTAAGAAACATTT---CTCTCTCAGATTTGTGACATAGACG 811  
 797 CTTACAAAAGAAATGGTCTCTCTTTGTGATGTAACCAATGCCCGAGTGTATCAATTTT 856  
 812 GAATCTGGGAGGACTCGAGACTTTGGCGCTGTATCACTTAAGAGCTACAATATT 871  
 857 ATGCTGAAGCATTTAATCTGTATGATGATTTATGCTTATCTGTGTATGATCTTACAT 916  
 872 ACATGATAGCATCGTCAACCTGTATGGCTTTGCTGGATTCCTGTGCTCTTACACG 931  
 917 CTTTAAAGCAGGAATTTGCTTTTGTTCAAAAGAGTGGTGGCAACATATGGTCAAT 976  
 932 TCTTCTACTGCAACAGTGTTCCTTTGTCGAGTGGAGGTGGCCACAGATGGTCACT 991  
 977 TTGCTGATGATTTCTCAAAAATATGAAGCATATGATCAATTTATTTTAAACA 1036  
 992 ATGCTGATAGATATCTCGGAAA---ACAAATGATGTGGCCAGAAATTTTATCTAGACA 1048  
 1037 CAGGTCCTTTTCCCATTTGCGGTGGAGCAAAATGCTGTGTTAACTCAGTGGAA 1096  
 1049 CTGGTGAATGTCAGTAAATTTGACGTTGGAGGTAAAGTATCTGTCACTGTCTGGAA 1108  
 1097 GCGAAGTCACTCAAGGACTGTCTTTCTGTGTAGGGGGGCAATGGGAAAACCTGGG 1156  
 1109 AAAAGGTAC---AGCACATACATAGTTTCTTTGTTCGGAATAAGAACTTAAGC 1165  
 1157 AGTTTGGCATTTGAGTGAACCTTGACCCAGGATGACTTACACAAATTAATTCGATG 1216  
 1166 AGTATGAATTTTCAAGGGCACTCTCAAAACAGATAGTACTCAATTTCAATGAATTTGACT 1225  
 1217 CAGATGTTAAGCTTGGAAACATTAACAGTGTTCAGTTTCACTCTGGAAAAAATTTGTTG 1276

Db 1226 CAGATGCGATGTTGGGACTTGCAGATGGTTAAATTTATTGGTATTAACAATGTGATCA 1285  
 QY 1277 AGATTTCTCAGATTAAGTTGGGAGCAGAAATGGTGTATAAATACATCTGGGAATATGAT 1336  
 Db 1286 ACCCAACTTACTAGTGGGAGCATCCAGATTTATAGTGAGAC-----AAATGTTGAA 1342  
 QY 1337 ATAAATCTACCTTCTGTAGCCAGACATTTATGGGACCTTAATATTCTCCAGAACCTGAAAC 1396  
 Db 1343 ACAGTTCAACTTCTGTAGTCAGAAACCGTCAGGAGGAAGTTCTGCTCACCTCACAC 1402  
 QY 1397 CATGCTA 1403  
 Db 1403 CGGTGTA 1409

RESULT 13  
 AAC98880  
 ID AAC98880 standard; cDNA; 1536 BP.  
 AC AAC98880;  
 XX  
 DT 09-MAR-2001 (first entry)  
 XX  
 DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:108.  
 XX  
 KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;  
 KW detection; diagnosis; identification; cytostatic; neuroprotective;  
 KW neoplastic; immunomodulatory; relaxant; contraceptive; gynaecological;  
 KW antiinflammatory; cardiac; gene therapy; chromosome mapping;  
 KW linkage analysis; tissue identification; tissue typing; forensic;  
 KW neural; immune system; muscular; reproductive; gastrointestinal;  
 KW pulmonary; cardiovascular; renal; proliferative; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055320-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05989.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-579444/54.  
 DR P-PSDB; AAB54115.  
 XX  
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
 PT treating, or ameliorating a medical condition, particular pancreatic  
 PT cancer, or for use in assays for diagnosing a pathological condition -  
 XX  
 PS Claim 1; Page 573; 1379pp; English.  
 XX  
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated  
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to  
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
 CC neuroprotective, neoplastic, immunomodulatory, relaxant, contraceptive,  
 CC gynaecological, cardiac and antiinflammatory activities, and can be used  
 CC in gene therapy. The polynucleotide and proteins can be used for  
 CC preventing, treating, or ameliorating a medical condition or in assays  
 CC for diagnosing a pathological condition or a susceptibility to one in a  
 CC subject. Binding partners to the proteins and the activity of the  
 CC proteins can be identified. The pancreatic cancer antigens can be used to  
 CC detect, treat or prevent pancreatic disorders, especially cancer.  
 CC Agonists and antagonists to the antigens can be screened for. The  
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
 CC acid hybridisation probes that can be used in chromosome mapping, linkage  
 CC analysis, tissue identification and/or typing and a variety of forensic  
 CC and diagnostic methods. The proteins can be used to generate antibodies  
 CC which are used to purify, detect and target the polypeptides, including

both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent sequences used in the exemplification of the present invention.

Sequence 1536 BP; 476 A; 321 C; 358 G; 380 T; 1 other;

ery Match 24.4%; Score 342.6; DB 21; Length 1536;  
 st Local Similarity 57.0%; Pred. No. 2.7e-86;  
 tches 791; Conservative 0; Mismatches 569; Indels 27; Gaps 8;

29 TGTCTTTGGCACATCAAGAGAAAGAGTTTCTATGAAGTTAGGGTGTTCCTCAAG 88  
 51 TGCTCTGGAGAGTAGCAGAGAAAGAGTTTCTACGAAGACTCGGTGCTCTCAGTG 110  
 89 ATGGTTTACCAATGACACAGGACTTTCTCAACAGAGTTGGTAGGTTTACCTGTCTCCAG 148  
 111 ATGACTCCCATGGTCAGGAATTACGGAAGAGACCCCTCCATATATTGGCTTGGTCTCCAA 170  
 149 AGAAGATAAACAACCTGGTTCTGCTCTACACTATACAAATCCCATGCTATCAGGAGA 208  
 171 AAGATGTCACACCCGCTTCTCTATATATCTATATGAGAACCCCAACAACTTTCAAGAAG 230  
 203 TCAGTGGCGTTAAATTTCTCAACTATCCAGGCTCATATTTTGAACAGACAGATCACCC 268  
 231 T---TGGCGAGATTCATCAGATCAGTGGCTCCAATTTCAAAACAAATGAAAACATC 287  
 269 GTATCAACATAGCTGGAT-----GGAACAGAGTGGCAATGGCAGAGACATGTGCA 322  
 288 GCTTTATTATTTCATGGATTTCATAGACAGGAGAGAGAAACTGGCTGGCCAAATGTGTGCA 347  
 323 ATGTGTTGCTACAGCTGAGATATAAATTCATTAATTTAGATTGSAATCAAGGTTTCAC 382  
 348 AGAATCTGTTCAAGTGGAGAGTGTGAATCTGTATCTGTGTGGACTGGAAGGTGGCTCCC 407  
 383 GG---GAATACATCCATCTGTAAACAATCCCGTGTGTGTGTGTGCTGAGGTGGCTTATT 439  
 408 GAACTGGATACACAAAGCTCGCAGAACATCAGGATCGTGGGAGCAGAGATGGCATATT 467  
 440 TTATTGATGTTCTCATGAAGAAATTTGAATTTCCCTTCTTAAGTGCACCTGATTTGGCC 499  
 468 TTGTTGAATTTCTTCAGTGGCGTTTCGGTTACTACCTTCCAAAGTGCATGATGGCC 527  
 500 ACAGCTTGGGAGCACACTGGCTGGGAGAGCTGGGTCAAGATACACAGG---CCTTGGAA 556  
 528 ACAGCTTGGTGGCCACGCTGCTGGGAGGCTGGAAGAGAACCAATGGACCATTTGGAC 587  
 557 GAATAACTGGGTTGGACCCAGCTGGCCATTTTTCACAACTCCAAAGAGAGTCAGGC 616  
 588 GCATCACAGGTTGGACCCAGCAGAACCTTGCTTTCAGGGGCACACCTGAATTAGTCCGAT 647  
 617 TAGACCCCTCGGATGCCAACTTTGTCAGCTTATTCATACAAATGCACTGCGATCCTCT 676  
 648 TGGACCCCGAGATGCCAAATTTGTGATGTATTCACAGGATGTGCCCCCATGATGCC 707  
 677 TTGAGCTTGGTGGAAACCAATGAGCTTGTGTGCTATTTTACCTTTTACCCAAATGGAG 736  
 708 CCAATTTGGGTTTGGAAATGAGCCAACTGCTGGGCCACCTAGATTTCCTTCCAAATGGAG 767  
 737 GGAAGCACATGCCAGGATGTGAAGACTTAATTACACTTTTACTGAAATTTAACTTCAATG 796  
 768 GAGTGGAAATGCTGGATGTAAAGAAACATTT---CTCTCAGATGTGGACATAGACG 824  
 797 CTTACAAAAGAAATGGCTTCTTCTTTGACTGTAAACCATGCCGGAAGTTATCAATTTT 856  
 825 GAATCTGGGAAGGACTCGAGACTTTGGCGCTGTATCACTTAAGAGCTACAAATATT 884  
 857 ATGCTGAAGCAATTTTAATCTGATGCAATTTATGCTTATCTTGTAGATCTACACAT 916  
 885 ACATGTATAGATCGTCAACCCCTGATGGCTTGTGGATTCCCTGTGCTCTTTCACAGC 944  
 917 CTTTAAAGCAGGAAATGCTTCTTTTGTTCAAAGAGAGTTTCCCAACAATGGGTCATT 976

Db 945 TCTTCACTGCAAAACAAGTGTTCCTTGTCCAAAGTGGAGGCTGCCACAGATGGTCACT 1004  
 Qy 977 TTGCTGATAGATTTCACCTTCAAAATATGAAGACTAATGGATCACTATTTTTTAAACA 1036  
 Db 1005 ATGCTGATAGATATCTTGGGAAA---ACAAATGATGTGGGCCAGAAATTTTATCTAGACA 1061  
 Qy 1037 CAGGTCCTCTTCCCAATTTGCCCATTTGGCGTTGGAGGCACAAATTTGTCTTAAACTCAGTGGAA 1096  
 Db 1062 CTGCTGATGCCAGTAATTTTGACAGTTTGAGGTTGAGGTATTAAGGTATCTGTACACACTGTCTGGAA 1121  
 Qy 1097 GCGAAGTCACTCAAGAACTGTCTTTCTTCTGTAGTGGCGGCAATTTGGGAAAACCTGGGG 1156  
 Db 1122 AAAAGGTTAC---AGGACACATACTAGTTTCTTTGTTCGAAATAAAGGAAACTCTTAAGC 1178  
 Qy 1157 AGTTTGCATTTGTCAAGTGGAAACTTTGAGCCAGGATGATCTTACACAAAATTAATCGATG 1216  
 Db 1179 AGTATGAAATTTTCAAGGCGACTCTCAACACAGATAGTACTCATTTCCATGATTTGACT 1238  
 Qy 1217 CAGATGTTAAGTGTGAAACATTAACAAGTGTTCAGTTCACTCTGGGAAAACATTTGTTTG 1276  
 Db 1239 CAGATGTGGATGTGGGACTTTGCAGATGTTTTAAATTTATTTGGTATTAACATGTGATCA 1298  
 Qy 1277 AAGATCTCAGAATAAGTTGGGAGCAGAAATGCTGATAAATACATCTGGGAAATATGGAT 1336  
 Db 1299 ACCCACTTTTACCTAGTGGGAGCATCCAGATTTATAGTGGAGAC---AAATGTTGAA 1355  
 Qy 1337 ATAACTACCTTCTGTAGCCAAAGACATTAATGGGACCTTAATTTCTCAGAACCTGAAAC 1396  
 Db 1356 AACAGTTCAACTTCTGTAGTCAGAAACCGTCAGGAGGAAAGTTCTGTCAACCTCACAC 1415  
 Qy 1397 CATGCTA 1403  
 Db 1416 CGTGTTA 1422

RESULT 14  
 AAS81083  
 ID AAS81083 standard; cDNA; 1410 BP.  
 XX AAS81083;  
 XX 13-FEB-2002 (first entry)  
 XX DNA encoding novel human diagnostic protein #16887.  
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX Homo sapiens.  
 XX WO200175067-A2.  
 XX 11-OCT-2001.  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX (HYSE-) HYSEQ INC.  
 XX Drmanac RT, Liu C, Tang YT;  
 XX WPI; 2001-639362/73.  
 DR P-PSDB; ABG16896.  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity  
 XX Claim 1; SEQ ID No 16887; 103pp; English.



The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

Sequence 1410 BP; 384 A; 320 C; 369 G; 337 T; 0 other;

Very Match 24.1%; Score 338; DB 23; Length 1410;  
 1st Local Similarity 54.9%; Pred. No. 5.2e-85;  
 Matches 778; Conservative 0; Mismatches 620; Indels 18; Gaps 5;

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1 ATGCTTGGAAATTTGATTTGTCATCTTCTTCTTGGCACATCAAGAGGAAAGAAGTT 60
1 ATGCTGCCCTTGGACCTGGCCCTTCTCTCTGCTGGCCACAGTCAGAGGAAAGAGTTC 60
61 TCGTATGAAGTTAGGTGTTTCAAGATGGTTTACATGGACACAGACTTTCTCAACA 120
61 TCGTACGACAACTTGGCTGCTTTTCTGATGAAACCATGGCGAGGAACTTCAGCGA 120
121 GAGTTGGTAGGTTTACCTGGTCTCCAGAGAGATAAACAATCGTTTCTGCTCACT 180
121 CCGTGAATAATTTACCTTCCCTGGTCCCGGAGACATTCACCCGCTTCTCTGTAC 180
181 ATACACATCCCAATGCCATTCAGAGATCAGTGGGTTAATTTCAACTATCCAGGCC 240
181 AATGAAATCCCAACAACTTCCACTAATCACTGGCACGGAACACAGACACATTGAGGCT 240
241 TCATATTTTGAACAGACAGATCAACCGATCAACATAGCTG-----ATGGAACA 294
241 TCAACTTCCACTGACCGGACAGACAGCTTCATCATCCATGCTTTTAGACAGGCG 300
295 GATGCCAATGGCAGAGACATGTGCAATGTGTTGCTACAGCTGGAAGATATAAATTGC 354
301 GAGGACAGCTGGCCATCGACATGTGCAAGAAATGTTTGAAGTGGAGAGGTGAACCTGC 360
355 ATTAATTTAGATTGATCAACGGTTCCAGGAA---TACATCCATGCTGTAAACATCTC 411
361 ATCTGTGGACTGAGGACCGGTCCCGGCAATGTACACCCAAAGCCGTGCAAAACATT 420
412 CCGTGTGTTGCTGAGTGGCTTATTTTATGATGTTCTCATGAAATAATTTGAATAT 471
421 CGGGTGTGTTGGGCGGAGACAGCTTCTTAATACAGCACTGTGCGAGCTAGGGTAC 480
472 TCCCTTCTTAAGTGCATTTGATTTGGCCACAGCTTGGAGCACACCTGGCTGGGAAGCT 531
481 AGCTTTGAGGACGTGTCATGTATCGGCCACAGCTTGGGCGCGCACACGCGCGGAGGCG 540
532 GGGTCAAGGATACAGAGCC---TTGGAAGATAACTGGGTTGACCCAGCTGGCCATT 588
541 GCGAGAGGCTGGGGGCGCGTGGGCGAGATCACAGGGCTGATTCAGCAGGCGCGTGC 600
589 TTCACACACTCCAAAGAGAGTCAAGCTAGACCCCTCGGATGCCAACTTTGTGACGTT 648
601 TTCCAGGATGAACCTGAGAGGTTTCGGTTGGATCCATCTGACCCGCTGTTTGTGGATGTG 660

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QY 649 ATTACATAAATGACAGTCGCATCTCTTTGAGCTTGGTGTGGAAACATGTGCTTGT 708
DB 661 ATTACACAGATTTCTTCCCATAGTTCCTTCCTTAGTTCGGAAATGAGCCAAAGGTG 720
QY 709 GGTCAATCTGACTTTTATCCCAATATGGAGGAGACACATGCCAGGATGTGAAGACTTAAT 768
DB 721 GGCCATCTGGATTTCTTCCAAATGGAGAAAGAAATGCCCGATGTAAAGAA---AAAT 777
QY 769 ACACCTTTACTGAAATTTAACTTCAATGCTTCAAAAAGAAATGGCTTCTTCTTTGAC 828
DB 778 GTCCCTTCAACATTTACTGATTAATGATGGAAATATGGGAAGAAATGTGTGTCT 837
QY 829 TGTAACTATGCCGAGTTATCAATTTTATGCTCAAAAGCATTTCTTAATCTGATGCAAT 888
DB 838 TGAATACCTAAGAAGCTTCGAGTATTACTCAAGCAGCGTCTCAACCTGATGGCTTC 897
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DB 958 GCTGAAGGATGCCCAAAATGGGCACTATGCTGACCAATTTAAGGGGAAA---ACAAGT 1014
QY 1009 ACTAATGATCACATTAATTTTAAACACAGGTCCTTTCCCATTTGCCCCGTTGGAGG 1068
DB 1015 GCTGTGGAACAAACCTTTTCTGGAACACAGGAGAGAGTGGTAACTTTACTAGTTGAGA 1074
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DB 1075 TATAGGTATCAGTCACACTTCTGGAAGAGAAAGTGAATGGGTACATCAGGATGCT 1134
QY 1129 GTAGCGGGGCAATTTGGGAAACTGGGGAGTTTGGCAATTTGCTAGTGGAAACCTTGAGCCA 1188
DB 1135 TTGATGGAAGTAAATGAAAACTCGAAACAATATGAGATTTTCAAGGATCCCTCAACCA 1194
QY 1189 GGCATGCTTACACAAATTAATCGATGACAGATGTTAACTGTTGGAACATTAACAAGTGT 1248
DB 1195 GATCGAAGTACAGCTGTGTATGATGTGGATTTTAAATGTTGGAATAATACAGAAGTT 1254
QY 1249 CAGTTCACTCTGGAATAAACATTTGTTTGAAGATTTCTCAGAAATGTTGGGAGCAGAAATG 1308
DB 1255 AAATTCCTCTGGAACAAACCTGGGATATAATCTATCTGAGCCCAACTGGGGCTTCCCA 1314
QY 1309 GTGATAATACATCTGGGAAATATGGATATAATCTACCTTCTGTAGCCAAAGACATATG 1368
DB 1315 ATCAGGTGCAAAAGTGGTGAAGATGGGACTGAGTATAATTTTGTAGCAGCAGACACTGTG 1374
QY 1369 GGACCTAATATTCTCCAGAACCTGAAACCATGCTAA 1404
DB 1375 GAAGAAACCTCTTGCATCTCTTTACCCCTTGTAA 1410

```

# RESULT 15

ABL69986  
 ID ABL69986 standard; DNA; 1450 BP.

XX ABL69986;

XX AC ABL69986;

XX DT 15-MAY-2002 (first entry)

XX DE Pancreas cancer related gene sequence SEQ ID NO:8323.

XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
 stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
 cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
 gene; ds.

XX OS Homo sapiens.

XX FN WO200194629-A2.

XX PD 13-DEC-2001.

30-MAY-2001; 2001WO-US10838.

05-JUN-2000; 2000US-209473P.  
05-JUN-2000; 2000US-209531P.  
18-SEP-2000; 2000US-233133P.  
18-SEP-2000; 2000US-233617P.  
20-SEP-2000; 2000US-234009P.  
20-SEP-2000; 2000US-234034P.  
20-SEP-2000; 2000US-234052P.  
22-SEP-2000; 2000US-234509P.  
22-SEP-2000; 2000US-234567P.  
25-SEP-2000; 2000US-234923P.  
25-SEP-2000; 2000US-234924P.  
25-SEP-2000; 2000US-235077P.  
25-SEP-2000; 2000US-235082P.  
25-SEP-2000; 2000US-235134P.  
25-SEP-2000; 2000US-235280P.  
26-SEP-2000; 2000US-235637P.  
27-SEP-2000; 2000US-235711P.  
27-SEP-2000; 2000US-235720P.  
27-SEP-2000; 2000US-235840P.  
27-SEP-2000; 2000US-235863P.  
28-SEP-2000; 2000US-236028P.  
28-SEP-2000; 2000US-236032P.  
28-SEP-2000; 2000US-236033P.  
28-SEP-2000; 2000US-236034P.  
28-SEP-2000; 2000US-236109P.  
28-SEP-2000; 2000US-236111P.  
29-SEP-2000; 2000US-236844P.  
29-SEP-2000; 2000US-236891P.  
02-OCT-2000; 2000US-237172P.  
02-OCT-2000; 2000US-237173P.  
02-OCT-2000; 2000US-237278P.  
02-OCT-2000; 2000US-237294P.  
02-OCT-2000; 2000US-237295P.  
02-OCT-2000; 2000US-237318P.  
03-OCT-2000; 2000US-237423P.  
03-OCT-2000; 2000US-237598P.  
03-OCT-2000; 2000US-237604P.  
03-OCT-2000; 2000US-237606P.  
03-OCT-2000; 2000US-237609P.  
01-NOV-2000; 2000US-244867P.  
01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
Soppet DR, Weaver Z;

WPI; 2002-189264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set -

Claim 1; SEQ ID 8323; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer.

CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
CC carcinoma, papillary carcinoma and Wilm's tumour.

SQ Sequence 1450 BP; 396 A; 326 C; 379 G; 349 T; 0 other;

Query Match 24.1%; Score 338; DB 24; Length 1450;  
Best Local Similarity 54.9%; Pred. No. 5.3e-85;  
Matches 778; Conservative 0; Mismatches 620; Indels 18; Gaps 5;

QY 1 ATGCTTGGAAATTGGATTGTTCATCTCTTCTTGGCACATCAAGAGGAAAGAGTT 60  
DB 1 ATGCTGCCCCCTTGGACCCCTCGCCCTCTCTCTGCGCCACAGTCAGAGAAAGAGGTC 60  
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DB 61 TGGTACGGACAACTTGGCTGCTTTCTGATGAAAAACCATGGCGAGGAACCCCTTCAGCGA 120  
QY 121 GAGTTGGTAGGTTTACCCCTGGTCTCCAGAGAGATAAACACTCGTTTCTGCTCTACACT 180  
DB 121 CCTGTAAATTTACTTCCCTGGTCCCCCGAGGACATGACACCGGCTTCTCTGTACACA 180  
QY 181 ATACAAATCCCAATGCTATCAGAGATCAGTGGGTTAATTTCTCACTATCOAGCC 240  
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QY 241 TCATATTTGGAAACAGACAAAGATCACCGGTATCAATAGCTGG-----ATGGAATA 294  
DB 241 TCAACTTCCNACTGGACCCAGACACGCTTCATCATCTGCTTCTTAGACAAGGG 300  
QY 295 GATGGCAATGGCAGAGAGACATGTGCAATGTGTTCTACAGCTGGAGATATAAATTGC 354  
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QY 412 GGT 471  
DB 421 CGGTTGT 480  
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QY 589 TTCCACACACTCCAAAGGAAGTCAGGCTAGACCCCTCGGATGCCCAACTTTGTTCAGCTT 648  
DB 601 TTCCAGGATGAACCTGAGGAGGTTGCGTTGGATCCATCTGACGCGGTGTGTGTGTGTGT 660  
QY 649 ATTATATAATGAGCTCCATCTCTTGTAGCTGGTGTGTGGACCACTGATGCTTGT 708  
DB 661 ATTCACAGAGATCTCTCTCCATAGTTCCTTCCCTAGGTTTCGGAATGAGCCAAAGGTG 720  
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DB 721 GGCCATCTGGATTCTTTCCAAATGGAGGAAGGAATGCCCGGATGTAAGAA---AAAT 777  
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QY 889 ATTGCTATCTTGTAGATCCTACATCTTTTAAAGCAGGAATGCTTCTTTTGTCTC 948  
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|||||  
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1369 GGACCTAATTTCTCCAGAACCTGAAACCATGCTAA 1404  
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1375 GAAGAAAAACGTTTGCAATCTCTTTACCCCTTGTTAA 1410  
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Maximum Match 100%

Listing first 45 summaries

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- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

t	Score	Query Match	Length	ID	Description
1	1404	100.0	1404	14	US-10-038-517-1
2	1402.4	99.9	2352	13	US-10-403-745-1
3	1399.4	99.7	1401	13	US-10-403-745-2
4	1234.6	87.9	1383	13	US-10-312-088-1
5	386.2	27.5	1481	10	US-09-969-347-193
6	342.6	24.4	1471	9	US-09-923-779-145
7	342.6	24.4	1471	10	US-09-969-347-176
8	342.6	24.4	1471	13	US-10-191-987-117
9	342.6	24.4	1536	9	US-09-925-297-108
0	338	24.1	1450	10	US-09-969-347-194
1	338	24.1	1506	9	US-09-925-297-280
2	224	16.0	938	9	US-09-923-779-139
3	209.2	14.9	907	9	US-09-923-779-76
4	204.2	14.5	879	9	US-09-923-779-94
5	203	14.5	963	9	US-09-923-779-22

Sequence 73, Appl  
Sequence 104, App  
Sequence 454, App  
Sequence 459, App  
Sequence 82, Appl  
Sequence 22, Appl  
Sequence 77, Appl  
Sequence 78, Appl  
Sequence 3160, Ap  
Sequence 3373, Ap  
Sequence 75, Appl  
Sequence 3414, Ap  
Sequence 3225, Ap  
Sequence 85, Appl  
Sequence 80, Appl  
Sequence 74, Appl  
Sequence 4353, Ap  
Sequence 3, Appl  
Sequence 3545, Ap  
Sequence 87, Appl  
Sequence 3573, Ap  
Sequence 88, Appl  
Sequence 96, Appl  
Sequence 103, App  
Sequence 101, App  
Sequence 4137, Ap  
Sequence 3387, Ap  
Sequence 3564, Ap  
Sequence 3568, Ap  
Sequence 4187, Ap

766 9 US-09-923-779-73  
872 9 US-09-923-779-104  
800 15 US-10-060-036-494  
789 15 US-10-060-036-459  
735 9 US-09-923-779-82  
633 9 US-09-925-297-22  
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764 9 US-09-923-779-78  
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567 15 US-10-060-036-3373  
789 9 US-09-923-779-75  
599 15 US-10-060-036-3414  
526 15 US-10-060-036-3225  
780 9 US-09-923-779-85  
741 9 US-09-923-779-80  
761 9 US-09-923-779-74  
659 15 US-10-060-036-4353  
55155 9 US-09-735-933-3  
524 15 US-10-060-036-3545  
752 9 US-09-923-779-87  
649 15 US-10-060-036-3573  
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748 9 US-09-923-779-96  
712 9 US-09-923-779-103  
743 9 US-09-923-779-101  
528 15 US-10-060-036-4137  
528 15 US-10-060-036-3387  
543 15 US-10-060-036-3564  
511 15 US-10-060-036-3568  
555 15 US-10-060-036-4187

## ALIGNMENTS

### RESULT 1

US-10-038-517-1  
; Sequence 1, Application US/10038517  
; Publication No. US20020115844A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Turner, C. Alexander Jr.  
; TITLE OF INVENTION: No. US20020115844A1 Human Lipase and Polynucleotides Encoding ti  
; FILE REFERENCE: LEX-0293-USA  
; CURRENT APPLICATION NUMBER: US/10/038,517  
; PRIOR FILING DATE: 2002-01-03  
; PRIOR APPLICATION NUMBER: US 60/259,830  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; US-10-038-517-1

Query Match 100.0%; Score 1404; DB 14; Length 1404;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCTTGAATTGGATTGTCATCTTCTTTGGCAGATCAAGAGGAAAGAGTT 60  
Db 1 ATGCTTGAATTGGATTGTCATCTTCTTTGGCAGATCAAGAGGAAAGAGTT 60  
QY 61 TCGTATGAAGGTAGGGTGTTCAGAGATGGTTTACATGGACGAGCTTCTCAACA 120  
Db 61 TCGTATGAAGGTAGGGTGTTCAGAGATGGTTTACATGGACGAGCTTCTCAACA 120  
QY 121 GAGTTGGTAGGTTTACCTCGTCTCCAGAGAGATAACACTCTCTTCTCTACACT 180  
Db 121 GAGTTGGTAGGTTTACCTCGTCTCCAGAGAGATAACACTCTCTTCTCTACACT 180  
QY 181 ATACATATCCATGCGCTATCAGAGATCAGTGGTGAATTTCTTCACTATCCAGGCC 240

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241 TCATATTTTGGACAGACAGATCACCGGTATCAACATAGCTGGATGGAACACAGATGGC 300  
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301 AAATGGCAGAGACATGTGCAATGTGTGCTCAGCTGGAAGATATAAATGCAATTAAT 360  
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361 TTAGATTGGATCAACGGTTACCGGAATACATCATCTGTAACATCTCCGTGTGTT 420  
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481 AAATGCACTTGAATGGCCAGCTTGGGAGCACCTGGCTGGGAACTGGGTCAAG 540  
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541 ATACAGGCTTGAAGAATAACTGGTTGGACCCAGCTGGGCCATTTTCCACAACT 600  
601 CCAAGGAAGTCAGCTAGACCTCGATGGCCAACTTTGACGTTATTCATCAAAAT 660  
601 CCAAGGAAGTCAGCTAGACCTCGATGGCCAACTTTGACGTTATTCATCAAAAT 660  
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661 GCAGCTGGCATCTCTTTGAGCTTGGTTGGAAACCAATGATCTTGTGCTCATCTTGAC 720  
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781 AAATTTAACTTCAATGCTTACAAAAGAAATGGCTTCTTTGACGTGAACCATGCC 840  
841 CGAAGTTATCAATTTATGCTGAAAGCAATCTTAATCTTGATGCAATTTATGCTTATCT 900  
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1081 GTTAAACTCAGTGGAGGCAAGTCACTCAAGGAATCTGCTTCTTCTGTTAGGGGGCA 1140  
1141 ATTGGGAAAACCTGGGAGTTTGCATTTGCTGGAATACTTGGAGCCAGGATGATTCAC 1200  
1141 ATTGGGAAAACCTGGGAGTTTGCATTTGCTGGAATACTTGGAGCCAGGATGATTCAC 1200  
1201 ACAAATTAATTCAGATCAGATGTTAAAGTTGGAACATTAACAGTGTTCAGTTCTG 1260  
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Db 1321 TCTGGGAAATATCGATATAAATCTACCTTCTGTAGCCAGACATTTATGGACCTAATATT 1380  
Qy 1381 CTCAGAACCTGAAACCATGCTAA 1404  
Db 1381 CTCAGAACCTGAAACCATGCTAA 1404

## RESULT 2

US-10-403-745-1  
; Sequence 1, Application US/10403745  
; Publication No. US20030165975A1  
; GENERAL INFORMATION:  
; APPLICANT: Khodadoust, Mehran  
; APPLICANT: Kapeller-Liebermann, Rosana  
; TITLE OF INVENTION: No. US20030165975A1 Human Lipase Proteins, Nucleic Acids Encod  
; FILE OF INVENTION: Them, and Uses of Both of These  
; FILE REFERENCE: 10147-14  
; CURRENT APPLICATION NUMBER: US/10/403,745  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US/09/411,132A  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2352  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (2159)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (2307)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (2313)  
; US-10-403-745-1

Query Match 99.9%; Score 1402.4; DB 13; Length 2352;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1403; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGGAAATTTGGATTGTGTCATCTTGTCTTTTGGCAATCAAGAGGAAAAAGATT 60  
Db 125 ATGCTTGGAAATTTGGATTGTGTCATCTTGTCTTTTGGCAATCAAGAGGAAAAAGATT 184  
Qy 61 TGCTATGAAAGGTTAGGTTGTTTCAAGATGTTTACCATGGACCGAGCTTTCTCAACA 120  
Db 185 TGCTATGAAAGGTTAGGTTGTTTCAAGATGTTTACCATGGACCGAGCTTTCTCAACA 244  
Qy 121 GAGTTGGTGGTTTACCCTGGTCTCCAGAGAGATAAACAATCGTTTCTGCTCTACACT 180  
Db 245 GAGTTGGTGGTTTACCCTGGTCTCCAGAGAGATAAACAATCGTTTCTGCTCTACACT 304  
Qy 181 ATACACAATCCCAATGCCCTATCAGAGATCAGTGGGTTAATTTCTCAACTATCCAGGC 240  
Db 305 ATACACAATCCCAATGCCCTATCAGAGATCAGTGGGTTAATTTCTCAACTATCCAGGC 364  
Qy 241 TCATATTTTGGAAACAGACAGATCACCGGTATCAACATAGCTGGATGGAACACAGATGGC 300  
Db 365 TCATATTTTGGAAACAGACAGATCACCGGTATCAACATAGCTGGATGGAACACAGATGGC 424  
Qy 301 AAATGGCAGAGACATGTGCAATGTGTGCTCAGCTGGAAGATATAAATGCAATTAAT 360  
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725 CCAAGGAGCTCAGCTACACCTCGATGCCAATCTTGTGTGACGTTATTCATCAAAAT 784  
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785 GCAGCTCGATCCTCTTTGAGCTTGGTGTGGACCAATGTATGCTGTGTCATCTTGAC 844  
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965 CGAAGTTATCAATTTATGCTGAAAGCAATCTTAATCCTGATGCAATTAATGCTTATCCT 1024  
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Publication No. US20030165975A1  
GENERAL INFORMATION:  
APPLICANT: Khodadoust, Mehran  
APPLICANT: Kapeller-Libermann, Rosana  
TITLE OF INVENTION: No. US20030165975A1el Human Lipase Proteins, Nucleic Acides Encodi  
TITLE OF INVENTION: Then, and Uses of Both of These  
FILE REFERENCE: 10147-14  
CURRENT APPLICATION NUMBER: US/10/403,745  
CURRENT FILING DATE: 2003-03-31  
PRIOR APPLICATION NUMBER: US/09/411,132A  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 2  
LENGTH: 1401  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-403-745-2

Query Match 99.7%; Score 1399.4; DB 13; Length 1401;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGAATTTGGATTGTTGTCATCTTCTTTGGCACATCAAGAGAAAAAGAGTT 60  
Db 1 ATGCTTGAATTTGGATTGTTGTCATCTTCTTTGGCACATCAAGAGAAAAAGAGTT 60  
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QY 241 TCATATTTTGGAAACAGACAAGATCAACCCGTATCAACATAGCTGGATGGAAAAACAGATGCG 300  
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Db 301 AAATGGCAGAGACATGTCATGTCATGTCAGTGGAGATATAAATGCAATTAAT 360  
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Db 421 GGTGCTGAGTGGCTTATTTTATGATGTTCTCATGAAAAAATTTGAAATATTTCCCTTCT 480  
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QY 541 ATACAGGCTTTGGGAAGATAAATCGGTGTGGACCCAGCTGGGCCATTTTCCACAACACT 600  
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QY 661 GCAGCTCGATCCTCTTTGAGCTTGGTGTGGAAACCAATGATGCTTGGTCTCTTGAC 720  
Db 661 GCAGCTCGATCCTCTTTGAGCTTGGTGTGGAAACCAATGATGCTTGGTCTCTTGAC 720  
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1021	CATTATTTTTTAAACACAGGGTCCCTTTCCCAATTTGCCGTTGGAGGCACAAAATGTCT	1080
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JT 4

J-312-088-1

Influence 1, Application US/10312088

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Agarwal, Parulaj

APPLICANT: Cogswell, John P.

APPLICANT: Kabinic, Karen S.

APPLICANT: Lai, Ying-Ta

APPLICANT: Martensen, Shelby A.

APPLICANT: Murdock, Paul R.

APPLICANT: Smith, Randall F.

APPLICANT: Strum, Jay C.

APPLICANT: Xiang, Zhaoxing

APPLICANT: Xie, Qing

APPLICANT: Rizni, Safia K.

[TITLE OF INVENTION: NOVEL COMPOUNDS

[LE REFERENCE: GP50029

PRELIMINARY APPLICATION NUMBER: US/10/312,088

PRELIM FILING DATE: 2002-12-20

PRELIM APPLICATION NUMBER: PCT/US01/19929

PRELIM FILING DATE: 2001-05-22

PRELIM APPLICATION NUMBER: 60/213,161

PRELIM FILING DATE: 2000-06-22

PRELIM APPLICATION NUMBER: 60/213,156

PRELIM FILING DATE: 2000-06-22

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; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-312-088-1

Query Match      87.9%; Score 1234.6; DB 13; Length 1383;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 69; Indels 18; Gaps 2;

QY 1 ATGCTTGGAATTTGGATTGTGCATTTCTTGTTCTTTGGCACATCAAGAGGAAAGAGATT 60
Db 1 ATGCTTGGAATTTGGATTGTGCATTTCTTGTTCTTTGGCACATCAAGAGGAAAGAGATT 60

QY 61 TCGTATGAAGAGTTAGGGTGTTCCTTCAAGATGTTTACCATGGACCGAGACTTTTCAACA 120
Db 61 TCGTATGAAGAGTTAGGGTGTTCCTTCAAGATGTTTACCATGGACCGAGACTTTTCAACA 120

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QY 241 TCATATTTTGGAAACAGACAGATGATCCCGTATCAACATAGCTGGATGGAACACAGATGGC 300
Db 241 TCATATTTTGGAAACAGACAGATGATCCCGTATCAACATAGCTGGATGGAACACAGATGGC 300

QY 301 AAATGGCAGAGAGACATGTGCCAATGTGTGCTACAGCTGGAGAGATATAAAATTCATTAAAT 360
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QY 361 TTAGATTGGATCAACGGTTTACCGGAAATACATCCATGCTGTAAACAATTCCTCGTGTGTT 420
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QY 481 AAAGTGCATTTGATTTGGCCACAGCTTTGGGACACACCTGGCTGGGAGAGCTGGGTCAAGG 540
Db 481 AAAGTGCATTTGATTTGGCCACAGCTTTGGGACACACCTGGCTGGGAGAGCTGGGTCAAGG 540

QY 541 ATACAGGCTTTGGAAGATAACTGGGTTGGACCCAGCTGGGCCATTTTCCACAACT 600
Db 541 ATACAGGCTTTGGAAGATAACTGGGTTGGACCCAGCTGGGCCATTTTCCACAACT 600

QY 601 CCAAGAAGGTCAGGCTAGACCCCTCGGATGCCAATTTGTTGAGCTTATTCATACAAT 660
Db 601 CCAAGAAGGTCAGGCTAGACCCCTCGGATGCCAATTTGTTGAGCTTATTCATACAAT 660

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QY 721 TTTTATCCCAATGAGGAGAGACATGCCAGAGATGTGAAGACTTAATTTACACCTTTACTG 780
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QY 781 AAATTTAACTTCAATGCTTACAAAAAGAAATGGCTTCTTTTGAATGTAACCATGCC 840
Db 781 AAATTTAACTTCAATGCTTACAAAAAGAAATGGCTTCTTTTGAATGTAACCATGCC 840

QY 841 CGAAGTATCAATTTTATGCTGAAAGCATTTCTTAATCCTGATGCAATTTATTTGCTTATCCT 900
Db 841 CGAAGTATCAATTTTATGCTGAAAGCATTTCTTAATCCTGATGCAATTTATTTGCTTATCCT 900

QY 901 TGATAGCTCACATCTTTTAAAGCAGGAAATTTGCTTTTGTGTCCAAAGAAAGAGTTCG 960

```





1252 TTCACTGGAAGAAACATTTGTTTGAAGATTCTCAGAAATAGTTGGAGCAGAAATGGTG 1311  
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1271 TTTCTTTGGAATAACAATGTGATAAATCCAACTCTCCCAAGTGGTGGCCCAAGATC 1330  
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1312 ATAATAATCTGGGAATATGGATATAAATCTACCTTCTGTAGCCAGCAAGATATGGGA 1371  
|||||  
1331 ACTGTGCAAAAGGAGAGAGAGACAGTGTACAACTCTGTAGCGAAGACACAGTGGG 1390  
|||||  
1372 COTAAATATCTCCAGAACTGAAACCACTGCTAA 1404  
|||||  
1391 GAAGACAGCTGCTCACCTCACCTCACCTGCTAA 1423  
|||||

LT 6

9-923-779-145  
quence 145, Application US/09923779  
tent No. US20020076721A1  
NERAL INFORMATION:  
PELLICANT: Pyle, Ruth A.  
PELLICANT: Xu, Jiangchun  
PELLICANT: Kalos, Michael D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
FILE REFERENCE: 210121.553  
CURRENT APPLICATION NUMBER: US/09/923,779  
CURRENT FILING DATE: 2001-08-06  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: FastSeq for Windows Version 4.0  
Q ID NO 145  
LENGTH: 1471  
TYPE: DNA  
ORGANISM: Homo sapiens  
9-923-779-145

ery Match 24.4%; Score 342.6; DB 9; Length 1471;  
st Local Similarity 57.0%; Pred. No. 1.5e-88;  
tches 791; Conservative 0; Mismatches 569; Indels 27; Gaps 8;  
  
29 TGTCTTTGGCAGATCAAGAGGAAAGATTTGCTATGAAAGTTAGGGTGTTCAAAG 88  
36 TGCTGTGGAGCAGTAGCAGGAAAGATTTGTACGAAAGACTCGGCTGCTCAGTG 97  
89 ATGGTTTACCATTGACCAAGAGATTTCTCAACAGAGTTGGTAGTTTACCCTGGTCTCCAG 148  
98 ATGACTCCCATGTCAGGAATACGGAAGAGCCCTCCATATTTGCTTGGTCTCCAA 157  
149 AGAAGATAAAGACTCGTTTCTGCTCTACACTATACAAATCCCAATGCCATATCAGGAGA 208  
158 AAGATGTCAACACCCGCTTCTCTATATATCTAATGAGAACCCAAACAACTTTCAAGAAG 217  
209 TCAGTGGGGTTAATCTTCAACTATCCAGCTCATATTTTGGAAACAGACAGATCACCC 268  
218 T---TGCGCAGATTATCAAGCATCAGTGGCTCCAAATTTCAAAACAAATAGAAAATC 274  
269 GTATCAACATAGCTGGAT-----GGAAACAGATGGCAATTTGGCAGAGACATGTGCA 322  
275 GCTTTATTATTATGATTCATAGACAAAGGAGAGAAAGTGGCTGGCCAATGTGTGA 334  
323 ATGTGTTGTACAGCTGGAAGATATAAATTTGCAATTAATTTAGATTGGATCAAGCTTAC 382  
335 AGAATCTGTTCAAGTGGGAAGTGTGAATGTATCTGTGTGACTGGAAAGTGGCTCCC 394  
383 GG---GAATACATCATCTGTGTAAACAAATCCGTTGTTGTTGCTGAGTGGGCTTATT 439  
395 GAATCGTATACACAGAGCTTCAGAAATCATCAGGATCGTGGGAGCAGAGTGGCATATT 454  
440 TTATTGATGTTCTCATGAAATAATTTGAATATTTCCCTTCTAAAGTGCATTTGATGGCC 499  
455 TTGTGTAATTTCTTCACTCGGCGTTGGTTTACTACCTTCCAAAGTGTGATGTCATTGGCC 514  
500 ACAGCTTGGGAGCACACTCGCTGGGAGAGCTGGGTCAAGGATACAGG---CTTGTGAA 556  
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Db 515 ACAGCTGGGTGCCACGCTGTCTGGGAGGCTGGAAGGAGAACCAATGGGACCATTTGGAC 574  
Qy 557 GAATAACTGGTTGGACCCAGCTGGGCCATTTTCCAACTCCAAAGGAAGTCAGGC 616  
Db 575 GCATCAGAGGTTGGACCCAGCAGAACCTTGTCTTCAGGGCAGACCTGAAATTAGTCCGAT 634  
Qy 617 TAGACCCCTCGGATGCAAACTTTGTTGAGCTTATTCATACAAATGACGCTCGCATCCTCT 676  
Db 635 TGGACCCACCGATGCCAAATTTGTGATGTAATTCACACGATGTTGGTCCCTCATAGTCC 694  
Qy 677 TTGAGCTTGTGTTGGAACCAATTTGATGCTGTGTGTCATCTTACCTTTTACCCAAATGGAG 736  
Db 695 CCAATTTGGGTTTGAATGAGCCAAAGTCTGGGCCACCTAGATTCTTTCCAAATGGAG 754  
Qy 737 GGAAGCACATGCCAGGATGTGAAGACTTAATACACCTTTACTGAAATTTAACTTCAATG 796  
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Qy 917 CTTTAAAGCAGGAAATGCTTCTTTTGTTCAAAGAGGTTGCCCAACAATGGGTCAAT 976  
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Qy 977 TTGCTGATGATTTCACTTCAAAATATGAAGACTAAATGGATCAGATTTATTTTAAACA 1036  
Db 992 ATGCTGATGATATCTCTGGGAAA---ACAAATGATGTGGGCCAGAAATTTTATCTAGACA 1048  
Qy 1037 CAGGGTCCCTTTTCCCATTTTGGCCGTTGGAGGCACAAATTTGCTTTAACTCAGTGGAA 1096  
Db 1049 CTGGTGTGTCAGTAAATTTTTCAGGTTGGAGGTATAAGGTATCTGTACACTGTCTGGAA 1108  
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Qy 1157 AGTTTCCCATTTGCTAGTGGAAACTTTGAGCCAGGAGTACTTACACAAATTAATCGATG 1216  
Db 1166 AGTATGAATTTTCAAGGCACTCTCAACACAGATAGTACTCATTTCCATGATTTGACT 1225  
Qy 1217 CAGATGTTAAGTGTGAAACATTAAGTGTTCAGTTCATCTGGAAGAAACATTTGTTTG 1276  
Db 1226 CAGATGTGATGTGGGACTTGCAGATGGTTAAATTTATTTGGTATTAACAAATGTGATCA 1285  
Qy 1277 AAGATTCTCAGAAATAGTTGGAGCAGAAATGGTGATAAATACATCTCGGAAATATGGAT 1336  
Db 1286 ACCCACTTTTCTAGTGGGAGGATCCAGATTATAGTGAGAC---AAATGTGGAA 1342  
Qy 1337 ATAAATCTACCTTCTGTAGCCAGACATTTAGGACCTPAATATTCTCCAGAACCTGAAAC 1396  
Db 1343 AACAGTTCAACTTCTGTAGTCCAGAAACCGTCAAGGAGGAAAGTTCTGTCTCACCCTCACAC 1402  
Qy 1397 CATGCTA 1403  
Db 1403 CGTGTTA 1409

RESULT 7

US-09-969-347-176  
; Sequence 176, Application US/09969347  
; Patent No. US2002011508A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-69  
; CURRENT APPLICATION NUMBER: US/09/969,347

RENT FILING DATE: 2001-10-02  
IOR APPLICATION NUMBER: US/60/237,598  
IOR FILING DATE: 2000-10-03  
IOR APPLICATION NUMBER: US/60/237,604  
IOR FILING DATE: 2000-10-03  
MEMBER OF SEQ ID NOS: 318  
FTWARE: Patent in version 3.0  
ID NO 176  
LENGTH: 1471  
YPE: DNA  
ORGANISM: Homo sapiens  
-969-347-176

ry Match 24.4%; Score 342.6; DB 10; Length 1471;  
t Local Similarity 57.0%; Pred. No. 1.5e-88;  
ches 791; Conservative 0; Mismatches 569; Indels 27; Gaps 8;

29 TGTCTCTTGGCAGCATCAAGAGGAAAGAGTTGCTATGAAGGTTAGGTTTCAAG 88  
38 TGTCTCTGGAGCAGTAGCAGGAAAGAAAGTTTGTACGAAGACTCGGCTGCTCAGTG 97  
89 ATGGTTTACCATGGACAGGACTTTCTCAACAGAGTTGGTAGTTTACCTGGTCTCCAG 148  
98 ATGACTCCCATGCTCAGGAATTTACGGAAGACCCTCCATATATTGCTTGGTCTCAA 157  
149 AGAGATAAACACTGCTTTCTGCTCTACACTATACAAATCCCAATGCCCTATCAGGAGA 208  
158 AAGATGCAACACCCGCTTCTCTCTATATCTAATGAGAACCCCAACAACTTTCAAGAAG 217  
209 TCAGTGGGTTAATTTCTCAATCTCAAGCCTCATATTTGGAAACAGACAAAGATCACCC 268  
218 T----TGCCCGCAGNTTCATCAAGCATCAGTGGCTCCAAATTTCAACAAATGAAGAACTC 274  
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275 GCTTTATTATTCATGGATTATAGACAGAGGAGAGAAACTGGCTGGCCAAATGTGCA 334  
323 ATGTGTTGTCTAGCTGGAGATATATATTTGATTTAGATGATCAACGGTTTCA 382  
335 AGAATCTGTTCAAGTGGAAAGTGTGAATCTGTGTGGAGCTGGAAAGGTGGCTCCC 394  
383 GG---GAATACATCCATGCTGTAACAACTCTCCGTGTTGTTGGTCTGAGGTGGCTTATT 439  
395 GAACCTGGATACACAAAGCCTCGCAGACATCAGGATCGTGGAGCAGAAAGTGGCAATT 454  
440 TTATTCATGTTCTCATGAAATTTGAATATCCCTTCTTAAGTGCACCTGATTTGGCC 499  
455 TTGTTGAATTTCTCAGTCGGCTTCCGTTACTCACTTCCAAACGTGCATGCTCATGGCC 514  
500 ACAGCTTGGAGCACACCTGGCTGGGGAAGCTGGGTCAAGGATACAGG---CCTTGGAA 556  
515 ACAGCTTGGTGGCCACGCTGTGGGAGGCTGGAGGAGAACCAATGGGACCAATTGGAC 574  
557 GAATACTGGTGGACCCAGCTGGGCCAATTTTCCAAACACTCCAAAGGAAGTCAAGC 616  
575 GCATCACAGGTTGGACCCAGCAGAACCTTGGTTTTCAGGGCACACCTGAATTTAGTCCGAT 634  
617 TAGACCCCTCGATGCCAATTTGTGAGTTTATTCACAAATGCACCTGCGATCTCT 676  
635 TGACCCCGCAGTGCACAAATTTGTGATGTAATTCACACGGATGGTCCCCCATAGTCC 694  
677 TTGAGCTTGGTGTGGAACCAATGTATGCTGTGGTCACTCTGACTTTTACCCAAATGGAG 736  
695 CCAATTTGGGTTTGAATGAGCAAGTGTGGGCCACCTAGATTTCTTTCCAAATGGAG 754  
737 GGAAGCAGATGCCAGATGAGACTTAATTAACCTTTTACTGAAATTTAATCTCAATG 796  
755 GAGTGAATGCTGTGATGTAAGAAACAACTT---CTCTCTCAGATTTGGACATAGAG 811  
797 CTTTACAAAAGAAATGGCTTCTCTTTTGTGACTGTAACCATGCCGGAAGTTATCAATTTT 856  
812 GAATCTGGGAGGAGCTCGAGACTTTCGGGCTGTATCACTTAAGAGACTACAAATTT 871

QY 857 ATGCTGAAAGCAATTCCTTAATCTGATGCAATTTATTGCTTATCCCTTTAGATCCCTACACAT 916  
Db 872 AACTGATAGCATCGTCAACCTGATGGCTTTGCTGGATCCCTCTGCTCTTACACAG 931  
QY 917 CTTTAAAGCAGGAAATTTGCTTTCTTTTCCAAAGAGGTTGCCCAACAAATGGGTCAAT 976  
Db 932 TCTTCACTGCAACCAAGTGTTCCTCTTGTCCAAAGTGGAGGCTGCCCAAGATGGGTCACT 991  
QY 977 TTGCTGATAGATTTCACTTTCAAAAATATGAAGACTAATGGATCACATTTATTTTAAACA 1036  
Db 992 ATGCTGATAGATATCTCTGGAAA--ACAAATGATGGGCCAGAAAATTTTATCTAGACA 1048  
QY 1037 CAGGTCCTCTTTCCCATTTGCCCTTTGGAGGCAAAATTTGTTTAAACTCAGTGGAA 1096  
Db 1049 CTGGTATGATCCAGTAAATTTGCACTTTGGAGGTATAAGGTATCTGTCACTGTCTGGAA 1108  
QY 1097 GCGAAGTCACTCAAGGACTGCTTTCTTCTGTTAGCGGGCAATTTGGGAAACTCGGG 1156  
Db 1109 AAAGGTTTAC---AGGACACATCTAGTTCTTTTGTTCGGAATTAAGGAAACTCTTAAGC 1165  
QY 1157 AGTTTGCCTATGTCAGTGGAAAACCTTGAGCCAGGCACTTACACAAAATTTAATCGATG 1216  
Db 1166 AGTATGAAATTTTCAAGGGCACTCTCAAAACAGATAGTACTCATTTCCAAATGAAATTTGACT 1225  
QY 1217 CAGATGTTAAAGTTGGAAAACATTACAGTGTTCAGTTTCATCTGGAAAAACATTTGTTG 1276  
Db 1226 CAGATGTTGATGTTTGGGACTTGCAGATGGTTAAATTTATTTGGTATTAACAATGTGATCA 1285  
QY 1277 AAGATTTCTCAGAAATTAAGTTGGAGCAGAAATGGTGAATAATACATCTGGGAAATATGAT 1336  
Db 1286 ACCCAACTTTTACCTAGCTGGAGCATCCAAGATTTAGTGGAGAC---AAATTTGGAA 1342  
QY 1337 ATAAATCTACCTTCTGTAGCCAAACATTAATGGACCTAATATTCTCCAGAACCTGAAAC 1396  
Db 1343 AACAGTTCAACTTCTGTAGTCCAGAAACCGTCAGGAGGAAGTTCTGCTCACCCTCACAC 1402  
QY 1397 CATGCTA 1403  
Db 1403 CGTGTA 1409

## RESULT 8

US-10-191-997-117  
; Sequence 117, Application US/10191997  
; Publication No. US20030207834A1  
; GENERAL INFORMATION:  
; APPLICANT: Oligos Etc., Inc.  
; APPLICANT: DALE, Roderic M. K.  
; APPLICANT: ARROW, Amy  
; APPLICANT: THOMPSON, Terry  
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their  
; FILE REFERENCE: 54800-5019  
; CURRENT APPLICATION NUMBER: US/10/191,997  
; PRIOR FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,820  
; PRIOR FILING DATE: 2001-07-10  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 117  
; LENGTH: 1471  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: NM\_000936  
US-10-191-997-117

Query Match 24.4%; Score 342.6; DB 13; Length 1471;  
Best Local Similarity 57.0%; Pred. No. 1.5e-88;  
Matches 791; Conservative 0; Mismatches 569; Indels 27; Gaps 8;  
QY 29 TGTCTTGGCAGCATCAAGAGGAAAGAGTTTCTATGAAGTTAGGTTGTTTCAAG 88

38 TGCTGCTGGGACGATAGCAGGAAAGAGTTTGTCTACGAAAGACTCGGTGCTTCAGTG 97  
89 ATGGTTTACATGGACAGGACTTTCTCAACAGAGTTGGTAGGTTTACCTGGTCTCCAG 148  
98 ATGACTCCCATGGTTCAGGAATTACGGAAGACCCCTCCATATATTGCCCTGGTCTCCAA 157  
149 AGAAGATAAACAACCTGGTTTCTGCTCTACACTATACAAATCCCAATGCCATCAGGAGA 208  
158 AAGATGTCAACACCCGGTCTCTCTATATATACTAATGAGAACCCCAACAACATTTCAAGAG 217  
209 TCAGTGGCGTTAATTTCTCACTATCCAGGCTCATATTTTGGNACAGACAGATCACCC 268  
218 T-----TGCACGAGATTCATCAAGCATCATGCGCTCCAAATTTCAAAACAATAGAAAAACTC 274  
269 GATCAACATAGCTGGAT-----GGAAAAACAGATGGCAATGGCAGAGACATGTGCA 322  
275 GCTTTATTATTATCATGGATTATAGACAGGAGAGAAACTGGCTGGCCCAATGTGTGA 334  
323 ATGTGTTCTACAGCTGGAAGATATAAATTCATTAATTTAGATTGGATCAACGGTTTCA 382  
335 AGAATCTGTTCAGGTGGAAGAGTGTGAACATGTATCTGTGTGGACTGGAAAGGTGGCTCCC 394  
383 GG--GAATACATCATCTCTCTAAACAATCTCCGTGTTGTTGTTGCTGAGTGGCTTATT 439  
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557 GAATAACTGGGTGGACCCAGCTGGGCCATTTTTCACAACTCTCCAAAGGAGTCAAGC 616  
575 GCATCACAGGCTGGACCCAGCAGAACCTTGTCTCAGGACACACCTGAATAGTCCGAT 634  
617 TAGACCCCTCGATGGCCCAACTTTCTGACGTTATTATACAAATGAGCTCGATCCTT 676  
635 TGGACCCAGCGATGCCAAATTTGTGATGTAAATTCACGGATGTGGCCCATAGTCC 694  
677 TTGAGCTTGGTGGACCACTGATGCTTGTGCTCATCTTGACTTTTACCCAAATAGGAG 736  
695 CCAATTTGGGTTTGGATGAGCCAGCTGCTGGGCCACCTAGATTCTTTCCAAATGGAG 754  
737 GGAAGCACATCCAGGATGTGAAGACTTAATTAACCTTTACTTGAATTTAACTTCAATG 796  
755 GAGTGGAAATCCCTGGATGTAAAGAAACATT---CTCTCTCAGATTGTGGACATAGAG 811  
797 CTTACAAAAAAGAAATGGCTTCTCTTCTGACTGTAAACCATGCCGAGTTATCAATTTT 856  
812 GAATCTGGGAGGACCTCGAGACTTTGGGCTGTATCACTTGAAGACTTACAAATATT 871  
857 ATGCTGAAGCAATCTTAATCTGATGCAATTAATGCTTATCCTTGTAGATCCTACACAT 916  
872 ACACGTATGATCGTCAACCCCTGATGGCTTGTGTAATTTCCCTGTGCTCTTCAACG 931  
917 CTTTAAAGCAGGAAATTTGCTTTCTTTTTCAAAGAGGTTGCCCAACATGGGTCATT 976  
932 TCTTCACTGCAACAGTGTTCCTTTGTCATAGTGGAGCTGCCACAGATGGGTCACT 991  
977 TTGCTGATPAGATTTCACTTCAAAATATGAAGACTAATGGATCACAATATTTTAAACA 1036  
992 ATGCTGATAGATATCTCTGGGAAA---ACAAATGATGTGGGCCAGAAATTTTATCTAGACA 1048  
1037 CAGGTCCTTTTCCCATTTGCCGTTGGAGGACAAATTTGCTGTAACTCACTGAGTGGAA 1096  
1049 CTGTGATGCGAGTAATTTTGCAGTTGGAGGTATAAGGTATCTGTCACTGTCTGGAA 1108  
1097 GCGAAGTCACTCAAGGAACATGCTTTCTTCTGCTAGCGGGGCAATTTGGAAAACTGGGG 1156  
1109 AAAAGGTTAC---AGGACACATACATAGTTCTTTTGTTCGGAAATAAAGAACTCTAAGC 1165

QY 1157 AGTTTGCATTTGTCAGTGGAAAACTTGAGCCAGGCATGACTTACACAAAAATTAATCGATG 1216  
DB 1166 AGTATGAATTTTTCAGGGCACTCTCAACACAGATAGTACTCATTCCAATGAATTTGACT 1225  
QY 1217 CAGATGTTAAGCTTGGAAAAATTAACAAGTGTTCAGTTCATCTGGAATAAATTTCTTTG 1276  
DB 1226 CAGATGTTGATGTTGGGCACTTGCAGATGGTTAAATTTATTGGTATAAATGATCA 1285  
QY 1277 AAGATTTCTAGATAAGTTGGGAGCAGAAATGGTGATATAATACATCTGGGAAATATGGAT 1336  
DB 1286 ACCCAACTTTTACCTAGAGTGGGAGCATCCAAGATTATAGTGGAGAC---AAATGTTGGAA 1342  
QY 1337 ATAATCTACTCTCTCTAGCCAAAGACATTATGGGACCTAATATTTCTCCAGAACCTGAAAC 1396  
DB 1343 AACAGTTCAACTTCTCTGTAGTCCAGAAACCGTCAAGGAGGAAGTTCTGCTCACCCCTCACAC 1402  
QY 1397 CATGCTA 1403  
DB 1403 CGTCTTA 1409

RESULT 9  
US-09-925-297-108  
; Sequence 108, Application US/09925297  
; Patent No. US20020081659A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA105  
; CURRENT APPLICATION NUMBER: US/09/925,297  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05989  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 928  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 108  
; LENGTH: 1536  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1482)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-297-108

Query Match 24.4%; Score 342.6; DB 9; Length 1536;  
Best Local Similarity 57.0%; Pred. No. 1.5e-88;  
Matches 791; Conservative 0; Mismatches 569; Indels 27; Gaps 8;  
QY 29 TGTTCTTTGGCACATCAAGAGGAAAGATTTTGTCTATGAAGGTTAGGGTGTTCAAAG 88  
DB 51 TGCTGTGGGAGCAGTAGCAGGAAAGAGTTTGTCTAGAAAGACTCGGCTGCTTCACTG 110  
QY 89 ATGTTTACCATGGACCCAGGACTTCTCAACAGAGTTGGTAGTTTACCTGGTCTCCAG 148  
DB 111 ATGACTCCCATGGTCAGGAATTACGGAAGACCCCTCCATATATTGCTTGGTCTCCAA 170  
QY 149 AGAAGATAAACAACCTGGTTTCTGCTCTACACTATACAAATCCCAATGCCATCAGGAGA 208  
DB 171 AAGATGTCAACCCCGCTTCTCTCTATATATCTAATAGAACCCCAACAACATTTCAAGAAG 230  
QY 209 TCAGTGGGTTAATTTCTTCAACTATCCAGCCCTCATATTTTGGAAACACAGATCACCC 268  
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QY 269 GTATCAACATAGCTGGAT-----GGAAAAACAGATGGCAATGGCAGAGACATGTGCA 322  
DB 288 GCTTTTATTATTCATGGAATTCATAGACAGGAGAGAAACTGCGTGGCCATGTGTGCA 347  
QY 323 ATGTTGTCTACAGCTGGGAAGATATAAATTTAGATTGAATCAACGGTTCAAC 382

348 AGAATCTGTTCAAGGTGGAAAGTGTGAACCTGTATCTGTGTGACTGGAAAGTGGCTCCC 407  
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 528 ACAGCTGGTGGCCAGCTGCTGGGGAGCTGGAGGAGAACCAATGGGACCAATGGAC 587  
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 588 GCATCACAGGTTGGACCCAGCAGAACCTTGTCTTCAGGCGACACCTGAATTAGTCCGAT 647  
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 648 TGACCCCAAGCATGCCAATTTGTTGATGTTAATTCACACGATGGTCCGCCCATAGTCC 707  
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 797 CTTACAAAGAAATGGCTCTCTTTTGTGCTGTGAACCAATGCCCGAGTTATCAATTTT 856  
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 857 ATGCTGAAGCAATCTTAATCTGTATGATTTTATGCTTATCTTGTAGATCTTACACAT 916  
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 1005 ATGCTGATAGATATCTGGGAA---ACAAATGATGTGGGCCAGAAATTTATCTAGACA 1061  
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 1179 AGTATGAAATTTCAAGGCACTCTCAAAACAGATAGTACTTCAATTCATGAATTTGACT 1238  
 1217 CAGATGTTAACTTGGAAACATTAAGTGTTCAGTCACTGGAAGAAACATTTGTTG 1276  
 1239 CAGATGTGATGTTGGGACTTGGCAGATGGTAAATTTATTTGATATAAACAATGTGATCA 1298  
 1277 AAGATTCTCAGAAATAGTTGGAGCAGAAATGGTGAATAATATACATCTGGGAAATATGGAT 1336  
 1299 ACCCAACTTTACTAGATGGGAGCATCCAGATTTATAGTGGAGC---AAATGTTGGAA 1355  
 1337 ATAAATCTACCTTCTGTAGCCAGACATATATGGACCTTAATTTCTCCAGAACTGAAAC 1396  
 1356 AACAGTTCAACTTCTGTAGTCCAGAAACCGTCAGGAGGAAGTTCTGCTCACCTCCACAC 1415  
 1397 CATGCTA 1403

Db 1416 CBTGTTA 1422

RESULT 10  
 US-09-969-347-194  
 ; Sequence 194, Application US/09969347  
 ; Patent No. US20020115085A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ebner, Reinhard  
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
 ; FILE OF INVENTION: Sets  
 ; FILE REFERENCE: 689290-69  
 ; CURRENT APPLICATION NUMBER: US/09/969,347  
 ; CURRENT FILING DATE: 2001-10-02  
 ; PRIOR APPLICATION NUMBER: US/60/237,598  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: US/60/237,604  
 ; PRIOR FILING DATE: 2000-10-03  
 ; NUMBER OF SEQ ID NOS: 318  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 194  
 ; LENGTH: 1450  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-969-347-194

Query Match 24.1%; Score 338; DB 10; Length 1450;  
 Best Local Similarity 54.9%; Pred. No. 3.2e-87;  
 Matches 778; Conservative 0; Mismatches 620; Indels 18; Gaps 5;

QY 1 ATGCTTGAATTTGGATTGTTGCATTTCTTTGGCACATCAAGGAAAGAAGTT 60  
 Db 1 ATGCTGCCCTTTGGACCTCGGCTTCTCTGCTGCCACAGTCAGAGGAAAGAGGTC 60  
 QY 61 TGTATGAAAGTTAGGTTGTTTCAAGATGTTTACATGGACCCAGGACTTTCTCAACA 120  
 Db 61 TGTACGACAACTTGGCTGCTTTCTGATGAAACCAATGGGCGAGAACCTTCACGGA 120  
 QY 121 GAGTTGGTAGTTTACCTGCTCTCCAGAGAAATAAACACTGTTTCTGCTCTACACT 180  
 Db 121 CCGTAAATTTACTTCCCTGCTCCCGAGACATTCACACCCGCTTTCTTCTGTACACA 180  
 QY 181 ATACAAATCCCAATGCTATCAGAGATCAGTGGGTAAATTTCTCAACTATCCAAGCC 240  
 Db 181 AATGAAATCCAAACACTTCCAACTAATCAGTGGACCGAACACACACCATTTGAGCT 240  
 QY 241 TCATATTTTGAACAGACAAGATCACCCGTATCAACATAGCTGG-----ATGGAACA 294  
 Db 241 TCAAACTTCCAACTGGACCGCAAGACACGCTTCATCATCCATGGCTTTTAGACAAGCG 300  
 QY 295 GATGGCAATGGCAGAGACATGTGCAATGTGTTGCTACAGCTGGAGATATAAATTGC 354  
 Db 301 GAGACAGCTGGCCATCGGACATGTGCAAGAAATTTTGAAGTGGAGAGGTGAACTGC 360  
 QY 355 ATTAATTTAGATTGGATCAACGGTTTCAACGGGAA---TACATCCATCTGTAAACAATCTC 411  
 Db 361 ATCTGTGTGACTGGAGGACGCGGTCCCGGCGCATGTACACCCCAAGCCGTGCAAACTT 420  
 QY 412 CGTGTGTTGTTGCTGAGGTGGCTTATTTTATTTGATGTTCTCATGAAAAAATTTGAATAT 471  
 Db 421 CGGTTGTTGGGGCGGAGACAGCTTTCTTAATCAAGACATGTGCGACGAGCTAGGTTAC 480  
 QY 472 TCCCTTTCTAAAGTGCATTTGATTGGCCACAGCTTGGGAGCACACCTGGCTGGGAAGCT 531  
 Db 481 AGCCTTGAGGACGTGCTATCGCCGACAGCTGGGCGGACACACGCCCGCGGAGGCG 540  
 QY 532 GGGTCAAGGATACACAGGCC---TTGGAAGAAATTAATCTGGTTGGACCCAGCTGGGCCATTT 588  
 Db 541 GGCAGGAGGCTGGGGGCGCGCTGGGCGAGGATCACAGGCTGGATCCAGCAGGCGCGTGC 600  
 QY 589 TTCCACACACTCCAAAGGAAGTCAGGCTAGACCCCTCGGATGCCAACTTTCTTGTGAGTT 648  
 Db 601 TTCAGGATGAACCTGAGGAGGTTGCGTTGGATGCTGATCCATCTGACCCGCTTTTGGATGTG 660

649 ATTCAATCAAAATGAGCTCGCATCTCTTTGAGCTTGGTGTGGAACCATGATGCTTGT 708  
661 ATTACACAGATTTCTTCCCATAGTCTCTTCCCTAGGTTTCGAATGAGCCAAAAGGTG 720  
709 GGTATCTTGTACTTTTACCCAAATGGAGGAGACACATGCGAGATGTGAAGACTTAATT 768  
721 GGCCATCTGGATTTCTTTCCAAATGGAGGAAGAAATGCCGGATGTAGAA--AAAT 777  
769 ACACCTTTTACTGAATTTAACTTCAATGCTTTACAAAAGAAATGGCTCTCTTTTGAC 828  
778 GTCCCTTCAACCATTTACTGATTAATGATGGAATATGGGAAGGAATTTGGTCTTGTCT 837  
829 TGTAAACCATGCCGAAGTTTCAATTTTATCTGAAAGCAATCTTAACTCTGATGATTT 888  
838 TGCAATCACTTAAGAGCTTCGAGTATTTACTCAAGCAGCGTCTCAACCTGATGCTTC 897  
889 ATTGCTTATCTGTAGATCTTACACATCTTTTAAAGCAGGAATGCTTTTCTTCC 948  
898 CTGGGCTATCCCTGTGCTCTACGATGAGTTTCAGGAGAGTAAGTGTTCCTCTGCTCA 957  
949 AAAGAAGGTTGCCCAACATGGGTCAATTTTGTGCTATAGATTTCACTTCAAAAATATGAG 1008  
958 GCTGAGAGATGCCCAAAATGGGCACTATGCTGACCAATTTAAGGGGAA--ACAAGT 1014  
1009 ACTAATGATCACATTTATTTTAAACACAGGGTCCCTTTTCCCATTTGCGGTTGGAGG 1068  
1015 GCTGTGGAACAAACCTTTTCTGAAACACAGGAGAGTGGTAACTTTACTAGTTGGAGA 1074  
1069 CACAAATTTCTGTTTAACTCAGTGGAGGAGAGTCACTCAAGGAAGTCTTTCTTCTGT 1128  
1075 TATAAGTATCAGTCACACTTTCTGGAAAGAGAAAGTGAATGGGTACATCAGGATTTGT 1134  
1129 GTAGCGGGGCAATTTGGAAACCTGGGAGTTTGGCCATTTGCTAGTGGAAAACCTTGAGCCA 1188  
1135 TTGTATGAACTAATGAAACTCGAAACAATATGAGATTTTCAAGAGATCCCTCAACCA 1194  
1189 GGCATGACTTACAAAATTAATCGATGAGATGTTAACTGTTGGAAACATTAACAGTGT 1248  
1195 GATGCAAGTCACTGCTGCTGATTTGATGTTGATTTTAAATTTTGGAAAAATACAGAAAGT 1254  
1249 CAGTTCTCTGAAAAACATTTCTTTGAAGATTTCTCAGAAATTAAGTTGGAGCAGAAATG 1308  
1255 AAATTTCTTGGACAAACCTGGGATAAATCTATCTGAGCCCAACTGGGGCTTCCCA 1314  
1309 GTGATAAATACATCTGGAAATATGGATATAAATCTACCTTCTGTAGCCCAACATTAATG 1368  
1315 ATCAGTGCAAAGTGTGGAATGGGACTGAGTATAAATTTTGTAGCAGCAGCACTGTG 1374  
1369 GGACTAATATTTCCAGAACCTGAAACCATGCTAA 1404  
1375 GAAGAAACGCTTGGCAATCTTTTACCTTTGTAA 1410

LT 11

9-925-297-280

tience 280. Application US/09925297

tent No. US20020081659A1

VERAL INFORMATION:

PPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: P4105

CURRENT APPLICATION NUMBER: US/09/925,297

PRIOR FILING DATE: 2001-08-10

RIOR APPLICATION NUMBER: PCT/US00/05989

RIOR FILING DATE: 2000-03-06

RIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: PatentIn Ver. 2.0

ID NO 280

LENGTH: 1506

TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-297-280

Query Match

Best Local Similarity 24.1%; Score 338; DB 9; Length 1506;

Matches 778; Conservative 0; Mismatches 620; Indels 18; Gaps 5;

QY 1 ATGCTTGAATTTGGATTTGTCATTTCTTTGTTCTTTGGCACAATCAAGAGAAAAGAGTT 60  
DB 27 ATGCTGCCCTTTGGACCTTCCGCTTCTCTGCTGCCACAGTTCAGAGAAAAGAGGTC 86  
QY 61 TGCATCAAAAGGTTAGGCTGTTTCAAAGATGGTTTACCATGGACACAGGACTTTCTCAACA 120  
DB 87 TGTACGGAACAATTGGCTGCTTTTCTGATGAAAAACCATGGCAGGAACCTTCAAGGA 146  
QY 121 GAGTTGGTATGTTTACCTGGTCTCCAGAGAGATAAACAACGTTTCTGTCTACACT 180  
DB 147 CTTGTAATAATTACTTCCCTGGTCCCGGAGGACATTTGACACCCGCTTTCTTCTGTACA 206  
QY 181 ATACACAATCCCAATGCTATCAGGAGATCAGTGGGTTAATTTCTTCAACTATCCAAGCC 240  
DB 207 AATGAATATCCAAACAACTTCCAACTAATCACTGGCAAGAAACACACACATTTGAGGT 266  
QY 241 TCATATTTTGGAAACACACAAGATCACCCGTATCAACATAGCTGG-----ATGGAACA 294  
DB 267 TCAAACTTCCAACTGGACCGCAAGACACGCTTTCATCCATGGCTTCTTAGACAAGGG 326  
QY 295 GATGGCAATATGGCAGAGACACATGTGCAATGTGTTGCTACAGCTGGAGATATAAATGTC 354  
DB 327 GAGGACAGCTGGCCATCGGACATGTCAAGAAATATGTTTGAAGTGGAGAGTGAAGTGC 386  
QY 355 ATTAATTTAGATTTGATCAACCGTTTCAACGGGAA---TACATCCATGCTGTAAACAATCTC 411  
DB 387 ATCTGTGTGACTGGAGGACACGCGTCCCGGCAATGTACACCAAGCGGTGCAAAACATT 446  
QY 412 CGTGTGTTGGTCTCAGTGGCTTATTTTATGATGTTTCTCATGAAAAAATTTGAATAT 471  
DB 447 CGGTTGTTGGGCGGAGACAGCTTTCTTAATACAGCACTGTGACCGCAGCTGGGGTAC 506  
QY 472 TCCCTTCTTAAAGTGCACTTTGATTTGGCCACAGCTTTGGGAGCACACCTGGCTGGGAGCT 531  
DB 507 AGCTTTGAGAGCTGATGTCATCGGCCACACCTTGGCGCGCCACACGCGCGGAGGG 566  
QY 532 GGTCTAAGGATACCAAGGCC---TTGGAAGAAATACTGGGTTGGACCCAGCTGGGCCATT 588  
DB 567 GGCAGGAGGCTGGGGGGCGCGTGGGACAGATCACAGGCTGATCCAGCAGCGCGCTGC 626  
QY 589 TTCCACAACACTCCAAAGGAAGTCAAGGCTAGACCCCTCGGATGCCCACTTTGTTGACGTT 648  
DB 627 TTCCAGATGAACCTGAGAGGTTGCTGTTGGATTCATCTGACCGCGTGTGTTGGATGTG 686  
QY 649 ATTCATACAAATGCACTCGCATCTCTTTGAGCTTGGTGTGGAAACCATTTGATGCTTGT 708  
DB 687 ATTCACACAGATTTCTTCCCATAGTTCTTCCCTAGGTTTCGGAATGAGCCAAAAGGTG 746  
QY 709 GGTCACTCTGACTTTTACCCAAATGGGGAAGACATGCCAGGATGTGAAGACTTAAT 768  
DB 747 GGCATCTGATTTCTTCCAAATGAGGAAGAAATGCCCGGATGTAGAA---AAAT 803  
QY 769 ACACCTTTACTGAATTTAACTTCAATGCTTACAAAAAGAAATGGCTTCTCTTTTGAC 828  
DB 804 GTCTTTTCAACCATTTACTGATATTTGATGGAATATGGGAAGGAATTTGGTGGCTTTGTGCT 863  
QY 829 TGTAAACATGCCGAAGTTTCAATTTTATGCTGAAGCAATTTCTTAATCTGTATGATGCT 888  
DB 864 TGAATACACTAAGAGCTTCGAGTATTACTCAACGACGCTCCCTCAACCTGATGGCTTC 923  
QY 889 ATTGCTTATCTCTGTAGATCTTACACATCTTTTAAAGCAGGAAATTTGCTTTTGTGTC 948  
DB 924 CTGGGCTATCCCTGTGCTCTTACGATGAGTTTCAGGAGAGTAAAGTGTTCCTTGTCCA 983  
QY 949 AAAGAAGGTTGCCCAACAATGGGTCAATTTTGTCTGTATGATTTTCACTTCAAAAATATGAG 1008

984 GCTGAAGGATGCCCAAAATGGGCACTATGCTGACCAATTTAAGGGGAAA---ACAAGT 1040  
 1009 ACTAATGGATCACAATTAATTTTAAACACAGGTCCTTTTCCCAATTTCCCGTTGGAGG 1068  
 1041 GCTGTGGAACAAACCTTTTCCCTGAAACACAGGAGAGAGTGGTAACTTTACTAGTTGGAGA 1100  
 1069 CACAAATTTGCTGTAACTCAGTGGAGGAGTCACTCAAGGAAGTGTCTTTCTTCTGCT 1128  
 1101 TATAAGGTATCAGTCACATTTCTGGAAGAGAAAGTGAATGAGGTACATCAGGAATGCT 1160  
 1129 GTAGGGGGCAATTTGGAAAACTGGGGAGTTTGCCATTTGTCAGTGGAAAACTTTCAGGCA 1188  
 1161 TTGTATGGAAGTAAATGAAACTCGAAACCAATATGAGATTTTCAAGAGTCCCTCAACCA 1220  
 1189 GGCATGACTTTACACAAATTAATCGATGAGATTTAAGCTTTGGAAAACTTACAAAGTGT 1248  
 1221 GATGCAAGTCACACGCTGTGCTATGATGAGATTTTAAATTTGGAAAAATACAGAAAGTT 1280  
 1249 CAGTTTCATCTGGAATAAAACATTTGTTTGAAGATTTCTCAGAAATAGTTGGAGCAGAAATG 1308  
 1281 AAATCTCTGGAACCAACGTTGGATAAATCTATCTGAGCCCAAACTGGGGCTTCCCAA 1340  
 1309 GTGATAAATACATCTGGAAATATGATGATATAATCTACCTTCTGTAGCCAAAGATTTATG 1368  
 1341 ATCAGAGTGAAGAGTGGTGAAGATGGGACTGAGTATATTTTGTAGCAGGCACACTGTG 1400  
 1369 GGCCTTAATTTCTCAGAACCTGAAACCATGCTAA 1404  
 1401 GAAGAAACGCTTGTGCAATCTCTTTACCCTTTGTTAA 1436

T 12

-923-779-139  
 uence 139, Application US/09923779  
 ent No. US20020076721A1  
 ERAL INFORMATION:  
 PLICANT: Pyle, Ruth A.  
 PLICANT: Xu, Jiangchun  
 PLICANT: Kalos, Michael D.  
 TLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 LE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
 LE REFERENCE: 210121.553  
 RENT APPLICATION NUMBER: US/09/923,779  
 RENT FILING DATE: 2001-08-06  
 MEER OF SEQ ID NOS: 155  
 FTWARE: FastSeq for Windows Version 4.0  
 ID NO 139  
 ENGT: 938  
 YPE: DNA  
 RGANISM: Homo sapiens  
 EATURE:  
 AME/KEY: misc feature  
 OCATION: 8, 16, 919, 929  
 THER INFORMATION: n = A,T,C or G  
 -923-779-139

ry Match 16.0%; Score 224; DB 9; Length 938;  
 t Local Similarity 59.8%; Pred. No. 3.6e-54;  
 ches 450; Conservative 1; Mismatches 286; Indels 15; Gaps 4;

29 TGTTCTTTGGCAGATCAGAGGAAAGTTTGTATGAAGAGTTAGGTTTAAAG 88  
 104 TGCTGTGGAGCAGTAGCAGGAAAGAGTTTGTACGAAAGACTCGGCTGCTCAGT 163  
 89 ATGGTTTACCATGGACAGGACTTTCTCAACAGAGTTGGTAGTTTACCCCTGGTCTCAG 148  
 164 ATGATCTCCCATGGTCAGGAATACGGAAGACCCCTCCATATATTGCTTGGTCTCAA 223  
 149 AGAGATAAAGACTGTTTCTGCTCTACATATACAAATCCCAATGCTTATCAGGAGA 208  
 224 AAGATGTCACACCCGCTTCTCCCTATATATTAATGAGAACCCCAACAACTTTCAAGAAG 283  
 209 TCAGTSCGGTTAATTTCTTCAACTACATCCAAAGCCTCATATTTTGGACACAGACATCACC 268

284 T---TGCCGAGATTCATCAAGCATCAGTGGCTCCAAATTTCAAAACAAATAGAAAACTC 340  
 269 GTATCAACATAGTGGAT-----GGAAACAGATGGCAAAATGGCAGAGACATGTGCA 322  
 341 GCTTTATTTATTCATGATTTATAGACAGGGAAGAAACACTGGCTGGCCCAATGTGTGCA 400  
 323 ATGTGTTGTACAGCTGGAGATATAAATTTGCAATTAATTTAGATTTGGATCAACGGTTTCA 382  
 401 AGAATCTGTTCAAGTGGAAAGTGTAACTGTATCTGTGTGACTGGAAAGTGGCTCCC 460  
 383 G---GGAATACATCCATGCTGTAAACAATCTCCGTTGTTGGTGTGCTGAGTGGCTTATT 439  
 461 GAATCTGATACACACAAGCTTCGCAAGCATCAGGATCTGGAGCAGAAAGTGGCATATT 520  
 440 TTATTGATGTTCTCATGAAAAAATTTGAATATTTCCCTTCTTAAAGTGACATTTGTTGGCC 499  
 521 TTGTTGAATTTCTTCAGTGGCGTTTCGGTTACTCACCTTCCAACTGATGTCTATTGGCC 580  
 500 ACAGCTTGGAGCACACCTGGCTGGGAGCTGGGTCAAGGATACCAAG---CCTTGGAA 556  
 581 ACAGCCTGGGTGCCACGCTGCTGGGAGGCTGGAAAGGAGAACCAATGGGACCATTTGAC 640  
 557 GAATAACTGGTTTGGACCCAGCTGGGCAATTTTCCCAACACACTCCAAAGGAAGTCAGGC 616  
 641 GCATCACAGGTTTGGACCCAGCAACCTTGTTCAGGGCACCCTGAAATTAGTCCGAT 700  
 617 TAGACCCCTCGGATCCCAACTTTGTTGACGTTATTATACAAATGACAGCTGCGATCCTCT 676  
 701 TGGACCCAGCAGCATGCCAAATTTTGGATGTAATTTACACGGATGGTGGCCCCATAGTCC 760  
 677 TTGAGCTTGTGTTGGAAACCATGATGCTTGTGCTGCTCATCTTGACTTTTACCAATGGAG 736  
 761 CCAATTTGGGGTTTGGATGAGCCAAATCTCGTGGGCCACCTAGATTTCTTTCCAAATGGAG 820  
 737 GGAAGCAGATGCCAGGATGTGAAGACTTTAAT 768  
 821 GAGTGAATGCTGATGTAAGAAAGACATT 852

RESULT 13

US-09-923-779-76/c  
 ; Sequence 76, Application US/09923779  
 ; Patent No. US20020076721A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pyle, Ruth A.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Kalos, Michael D.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
 ; FILE REFERENCE: 210121.553  
 ; CURRENT APPLICATION NUMBER: US/09/923,779  
 ; CURRENT FILING DATE: 2001-08-06  
 ; NUMBER OF SEQ ID NOS: 155  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 76  
 ; LENGTH: 907  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 23, 104, 110, 763, 786, 792, 819, 822, 834, 836, 842, 843,  
 ; LOCATION: 892, 900  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-923-779-76

Query Match 14.9%; Score 209.2; DB 9; Length 907;  
 Best Local Similarity 59.0%; Pred. No. 7.2e-50;  
 Matches 434; Conservative 0; Mismatches 286; Indels 15; Gaps 4;  
 QY 46 AGAGAAAGAAAGTTTGTATGAAGGTTAGGGTGTTCCTTCAAGATGTTTACCATGACC 105  
 DB 771 AGGAAAAAAGTTTGTACGAAAGACTCGGCTGCTTCAATGATGACTCCCATGGTCA 712

106 AGGACTTCTCAACAGAGTTGGTAGTTTACCTGGTCTCCAGAGAGATAAACAACCTGCT 165  
 711 GAATTAACGGGAAGACCCCTCCATATATGGCTTGGTCTCCAAAGATGTCAACACCCGC 552  
 166 TTCTGCTCTACACTATACAAATCCCAATGCCATCAGAGATCAGTGGGTTAATCT 225  
 651 TTCTCTCTATATCTAATAGAACCCCAACAACATTTCAAGAAGT---TGCCGAGATTCA 595  
 226 TCAACTATCCAAAGCTCATATTTTGGAAACAGACAGATCACCGTATCAACATAGCTGA 285  
 594 TCAAGCATCACTGGCTCCATTTCAAACAAATAGAAAACCTGGCTTTATTTATCATGA 535  
 286 T-----GGAAAAACAGATGGCAATGGCAGAGACATGTGCAATGTGTGTACAGTG 339  
 534 TTCTAGACAAAGGAGAGAAATCTGGCTGGCAATGTGTGCAAGAATCTGTTCAGAGTG 475  
 340 GAAGATATAAATTCATTAATTTAGATGGATCAACGGTTACG---GGAAATACATCCAT 396  
 474 GAAGTGTGAATCTGTATCTGTGTGACTGGAAGGTGGCTCCCGAACTGGATACACAA 415  
 397 GCTGTAAACAAATCCCGT 456  
 414 GCCTCGCAGACATCAGGATCGTGGGAGCAGAGTGGCATATTTTGTGAAATTTCTTCAG 355  
 457 AAAAAATTTGAATATTTCCCTTCTAAAGTGCATTTGATGGCAGACAGCTTGGAGCAGAC 516  
 354 TCGGCTTGGGTTTACTCACCTTCCAACTGCAAGTGTGATTTGGCCACAGCTGGGTGCCAC 295  
 517 CTGGCTGGGGAAGCTGGGTCAAGATACACAG---CCTTGGAAAGATAACTGGGTTGGAC 573  
 294 GCTGTGGGAGGCTGGAAGAGAACCAATGGGACCATTTGACGCATCAGGGTTGGAC 235  
 574 CCAGCTGGGCATTTTCCACACACTCMAAGAGAGTGGGTAGGCTAGACCCCTCGGATGCC 633  
 234 CCAGCAGAACCTTCTTTCAGGGCAGACCTGAATTTAGTCCGATTGGACCCACGCGATGCC 175  
 634 AACTTTGTGAGCTTATTCATACAAATGCAGCTGCGATCCTCTTTGAGCTTGTGTGGA 693  
 174 AAATTTGTGATGAATTCACACGGATGGTGGCCCATAGTCCCAATTTGGGTTTGA 115  
 694 ACCATTGATGCTGTGTGCTATTGATCTTTTACCCAAATGGAGGAGCAGATGCCAGGA 753  
 114 ATGACCAAGNCGTGGGCGACCTAGATTTCTTTCCAAATGGAGGAGTGGAAATGCCCTGA 55  
 754 TGTGAAGACTTAAT 768  
 54 TGTAAAAAGAACATT 40

LT 14  
 9-923-779-94/c  
 quence 94, Application US/09923779  
 tent No. US20020076721A1  
 NERAL INFORMATION:  
 PPLICANT: Pyle, Ruth A.  
 PPLICANT: Xu, Jiangchun  
 PPLICANT: Kalos, Michael D.  
 TLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 TLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
 ILE REFERENCE: 210121.553  
 URRENT APPLICATION NUMBER: US/09/923,779  
 URRENT FILING DATE: 2001-08-06  
 UMBER OF SEQ ID NOS: 155  
 FTWARE: FastSeq for Windows Version 4.0  
 Q ID NO 94  
 LENGTH: 879  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 106, 111, 649, 711, 779, 788, 808, 811, 812, 817, 820, 825,  
 LOCATION: 845, 851

OTHER INFORMATION: n = A,T,C or G  
 US-09-923-779-94

Query Match 14.5%; Score 204.2; DB 9; Length 879;  
 Best Local Similarity 58.8%; Pred. No. 28-48;  
 Matches 443; Conservative 0; Mismatches 294; Indels 16; Gaps 5;  
 QY 29 TGTCTTTGGCAGATCAAGAGGAAAGAGATTTGGTATGAAAGGTTAGGGTGTTCAA-A 87  
 DB 790 TCNTGCTGGGAGCAGTAGCAGAAAAGAGATTTGTACGAAAAGACTCGGCTGCTTCAAGT 731  
 QY 88 GATGGTTTACCTAGGACCGAGACTTTCTCAACAGAGTTGGTAGGTTTACCTGGTCTCCA 147  
 DB 730 GATGACTCCCATGGTGCAGNAATTTACGGAAGACCCCTCCATATATTGCTTGGTCTCCA 671  
 QY 148 GAGAAGATAAACAACCTCGTTTCTGCTCTACATATACACAATCCCAATGCCCTATCAGAG 207  
 DB 570 AAGATGTCAACACCGCTTCTCTCTATATATATATGAGAACCCCAACAACCTTCAAGAA 611  
 QY 208 ATCAGTGGGTTTAAATCTTCAACTATCCAAAGCTCATATTTTGGAAACAGACAAAGATCAC 267  
 DB 610 GT---TGCCGCGAGATTCATCAAGCATCAGTGGCTCCAAATTTCAAAACAAATAGAAAAACT 554  
 QY 268 CSHATCAACATACCTCGAT-----GGAAAAACAGATGGCAATGGCAGAGACATGTGC 321  
 DB 553 CGCTTTATTTTCAATGATTCATAGCAAGGAGAGAAACTGGCTGGCCATGTGTGC 494  
 QY 322 AATGTGTGTCTACAGCTGGAAGATATAAATTCATTAATTTAGATTGGATCAACGGTTCA 381  
 DB 493 AAGAAATCTGTTCAAGGTGGAAGTGTGAACTGTATCTGTGTGAGCTGGAAAGGTGGCTCC 434  
 QY 382 CG---GGAATACATCCATCTGTAAACATCTCCGTGTGTGTGTGTGTGTGTGTGTGTGT 438  
 DB 433 CGAACTGGATACACACAGCTCGCGAAGAACATCAGATCTGTGGAGCAGAGTGGCATAT 374  
 QY 439 TTTATTGATGTTCTCATGAAAAATTTGAAATTTCCCTTCTTAAAGTGCACATTGATGGC 498  
 DB 373 TTTGTTGAATTTCTTCAGTGGGTTGCGTTTACTCACTTCCACGTCATGTCTATTGGC 314  
 QY 499 CACAGCTTGGGACACACCTGGCTGGGAGCTGGGTCAAGATACACAG---CCTTGA 555  
 DB 313 CACAGCTGGGTGCCACCGCTGTGGGAGGCTGGAAGAGAAACCAATGGGACCAATTGGA 254  
 QY 556 AGAATAACTGGGTGGACCCAGCTGGGCCATTTTCCCAACACATCCCAAGGAAGTCAAG 615  
 DB 253 CGCATCACAGGTTGACCCAGCAGAACCTTCTTTCAGGGCACACCTGAATTAGTCCGA 194  
 QY 616 CTAGACCCCTCGGATGCCAACTTTGTGAGCTTATTCATAAATGCGAGCTCGCATCTC 675  
 DB 193 TTGGACCCCGAGCGATGCCAAATTTGTGGATGTAATTCACAGGATGGTGGCCCATAGTC 134  
 QY 676 TTTGAGCTTGGTGGAAACCATTTGATGCTTGTGCTCATCTTGTACTTTTACCAATGGA 735  
 DB 133 CCCAATTTGGGTTTGGATGANCCAATCTGTGGCCACCTAGATTTCTTCCAAATGGA 74  
 QY 736 GGAAGACATGCTCAGGATGTGAAGACTTAATT 768  
 DB 73 GGAAGTGAATGCTGATGTAAAGAAACATT 41

RESULT 15  
 US-09-923-779-22/c  
 ; Sequence 22, Application US/09923779  
 ; Patent No. US20020076721A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pyle, Ruth A.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Kalos, Michael D.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
 ; FILE REFERENCE: 210121.553  
 ; CURRENT APPLICATION NUMBER: US/09/923,779  
 ; CURRENT FILING DATE: 2001-08-06

MEMBER OF SEQ ID NOS: 155  
SOFTWARE: FastSeq for Windows Version 4.0  
ID NO 22  
LENGTH: 963  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 26, 39, 40, 43, 44, 46, 54, 57, 948, 956  
OTHER INFORMATION: n = A,T,C or G  
-923-779-22

try Match 14.5%; Score 203; DB 9; Length 963;  
t Local Similarity 59.9%; Pred. No. 4.8e-48;  
ches 452; Conservative 0; Mismatches 285; Indels 18; Gaps 6;

29 TGTCTTTTGGCAGATCAAGAGAAAGAGTTTGTCTATGAAAGTTAGGGTGTTCRAAG 88  
|||  
860 TGTCTGTTGGAGAGTAGCAGGAAAGAGTTTGTCTACGNAAGACTCGCTGCTTCAGTG 801  
|||  
89 ATGGTTTACCATGGACAGAGCTTTCTCAACAGAGTTGGTAGGT-TTACCCCTGGTCTCCA 147  
|||  
800 ATGACTCCCCCATGGTTCAGGAATTACGGAAAGAGCCCTCCATATATTGCTTGGTCTCCA 741  
|||  
148 GAGAAGATAAACAAGCTGTTCTCTCTCTACATATACACAATCCCAATGCCATACAGAG 207  
|||  
740 AAGATGTCACACACCGCTTCTCTCTATATATCTAATAGAACCCCAACAACCTTTCAAGAA 681  
|||  
208 ATCAGTGGCGTTAATCTTCAACTATCCAGCGCTCATATTTTGGAAACAGACAAGATCACC 267  
|||  
680 GT---TGCCGAGATTTCATCAAGCATCAGTGGCTCCAAITTCAAACAAATAGAAAACT 624  
|||  
268 CGTATCAACATAGCTGGAT-----GGAAAAAGATGGCAATGGCAGAGAGACATGTGC 321  
|||  
623 CGCTTTATTATTTCATGGATTCATAGACAAGGAGAGAAAACTGGCTGGCCCAATGTGTGC 564  
|||  
322 AATGTGTGTGTACAGCTGGAAGATATAAATTTGCATTAAITTTAGATTGGATCAACGGTTCA 381  
|||  
563 AAGAACTGTTCAGGTGGAGAGTGTGAATCTGTGTGACTGGAAAGGTGGCTCC 504  
|||  
382 CG---GGAATACATCCATGCTGTAAACAATCTCCGTTGTTGGTGTGCTGAGGTGGCTTAT 438  
|||  
503 CGAACTGGATACACACAAGCTCGCAGAACATCAGGATCGTGGGAGCAGAAAGTGCCATAT 444  
|||  
439 TTTATTGATGTTCTCATGAAAAAATTTGAATATCCCTTCTTAAGTGCACCTTGATTGGC 498  
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ime : 486 secs



GenCore version 5.1.6  
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US-10-038-517-1

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Listing first 45 summaries

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17: em\_hum:\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1404	100.0	1404	6	AX544122	AX544122 Sequence
2	1402.4	99.9	2352	6	AR310490	AR310490 Sequence
3	1402.4	99.9	2374	9	HS0804731	AL833418 Homo sapi
4	1399.4	99.7	1401	6	AR310491	AR310491 Sequence
5	1115.8	75.5	1526	6	AX535973	AX535973 Sequence
6	808	57.5	1540	6	AX405998	AX405998 Sequence
7	386.8	27.5	1493	4	DOGPLIP	M35302 Canine lipa
8	386.2	27.5	1481	6	AX337813	AX337813 Sequence
9	386.2	27.5	1481	9	HUMLRP1P	M93283 Human pancr
10	386.2	27.5	1513	9	BC025784	BC025784 Homo sapi
11	376.2	26.8	1443	4	ECPL	X66218 E. caballus
12	373.4	26.6	1620	10	AF061274	AF061274 Mus muscu
13	370.2	26.4	1534	10	RNLAPRNA	X61925 R. norvegicu
14	345.8	24.6	2338	10	AF177402	AF177402 SpermoPhi
15	344.2	24.5	1846	10	AF395870	AF395870 SpermoPhi
16	344.2	24.5	1848	10	AF027293	AF027293 SpermoPhi
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ACCESSION	AX544122				
VERSION	AX544122.1	GI:25277625			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Yu, X. and Turner, C.A.				
AUTHORS	Human lipase and polynucleotides encoding the same				
TITLE	Patent: WO 02053753-A 1 11-JUL-2002;				
JOURNAL					

Lexicon Genetics Incorporated (US)

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ACCESSION AR310490  
VERSION AR310490.1 GI:31703471  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2352)  
AUTHORS Khodadoust,M. and Kapeller-Libermann,R.  
TITLE Human lipase proteins, nucleic acids encoding them, and uses of  
JOURNAL Patent: US 6558936-A 1 06-MAY-2003  
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VERSION
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 2374)
AUTHORS
Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
TITLE
Direct Submission
JOURNAL
Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKEZp313P1022) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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LOCUS Sequence 2 from patent US 6558936.  
DEFINITION AR310491  
ACCESSION AR310491  
VERSION AR310491.1 GI:31703472  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 1401)  
AUTHORS Khodadoust, M. and Kapeller-Libermann, R.  
TITLE Human lipase proteins, nucleic acids encoding them, and uses of both of these  
JOURNAL Patent: US 6558936-A 2 06-MAY-2003;  
FEATURES Location/Qualifiers  
source 1..1401  
BASE COUNT 411 a 274 c 304 g 412 t  
ORIGIN  
Query Match 99.7%; Score 1399.4; DB 6; Length 1401;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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	ON	AX535973.1 GI:25262503			
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ANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1					
ENCE	Harland L., Arvizu, C., Das, D., Griffin, J.A., Baughn, M.R., Ding, L.,				
HORS	Walia, N.K., Yao, M.G., Lu, Y., Elliott, V.S., Thangavelu, K.,				
	Ramkumar, J., Lai, P.G. and Tribouley, C.M.				
LE	Lipid metabolism enzymes				

JOURNAL	Patent: WO 0229036-A 12.11-APR-2002;					
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 AX405998  
 AX405998.1 GI:21439435  
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 Tang, X.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F.,  
 Xue, A.J., Yang, Y., Wehrman, T. and Drmanac, R.T.  
 Novel nucleic acids and polypeptides  
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 ACCESSION M35302  
 VERSION M35302.1 GI:164047  
 KEYWORDS lipase.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
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 1 (bases 1 to 1493)  
 Korflec, B., LaForge, K.S., Puigserver, A. and Scheele, G.  
 Primary structures of canine pancreatic lipase and phospholipase A2  
 messenger RNAs  
 JOURNAL Pancreas 1 (5), 430-437 (1986)  
 MEDLINE 87175472  
 PUBMED 3562437

INT Original source text: Canine pancreas, cDNA to mRNA.  
 Draft entry and computer-readable [or printed] sequence for [1]  
 kindly submitted by G.Scheele, 06-MAR-1990.

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 ORGANISM Homo sapiens  
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 Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,  
 Horrigan,S., Soppet,D.R. and Weaver,Z.

LE Cancer gene determination and therapeutic screening using signature

Gene sets

Patent: WO 0194629-A 8322 13-DEC-2001;

Avalon Pharmaceuticals (US)

Location/Qualifiers

source

1. .1481

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Local Similarity 57.1%; Pred. No. 5.3e-83;

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121 GAGTGTGAGTTTACCCCTGGTCTTCAGAGAGATAAACACTCGTTTCTGCTTACACT 180

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620 GAGATCTCTGAGAGGTGCGACTTGTATCCCTCTGATGCTGACTTTGTTGATGATT 679

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RESULT 9

HUMLRP1P 1481 bp mRNA linear PRI 07-JAN-1995

LOCUS Human pancreatic lipase related protein 1 (PLRP1) mRNA, complete cds.

DEFINITION

ACCSSION M3283

VERSION M3283.1 GI:187229

KEYWORDS lipase related protein 1.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1481)

AUTHORS Giller, T., Buchwald, P., Blum-Kaelin, D. and Hunziker, W.

TITLE Two novel human pancreatic lipase related proteins, hPLRP1 and hPLRP2. Differences in colipase dependence and in lipase activity

JOURNAL J. Biol. Chem. 267 (23), 16509-16516 (1992)

MEDLINE 92355622

PUBMED 1379598

COMMENT Original

FEATURES

source

Location/Qualifiers

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## RESULT 10

BC025784

## LOCUS

DEFINITION

IMAGE:5226231, mRNA, complete cds.

ACCESSION

BC025784

VERSION

BC025784.1 GI:19343957

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1513)

Strausberg, R.

Direct Submission

Submitted (06-MAR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

BC025784 1513 bp mRNA linear PRI 11-MAR-2002  
Homo sapiens, pancreatic lipase-related protein 1, clone MGC:34434  
IMAGE:5226231, mRNA, complete cds.

BC025784  
BC025784.1 GI:19343957  
MGC.

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1513)  
Strausberg, R.  
Direct Submission  
Submitted (06-MAR-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc\_mg@hghri.nih.gov  
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,  
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,  
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 McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,  
 Tongson, E.E., Touchman, J.W., Teurigne, C., Vogt, J.L., Walker, M.A.,  
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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HORS Sequence of horse pancreatic lipase as determined by protein and  
LE cDNA sequencing. Implications for p-nitrophenyl acetate hydrolysis  
by pancreatic lipases  
Eur. J. Biochem. 206 (1), 279-287 (1992)  
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J. 12

274  
 HITON Mus musculus pancreatic lipase related protein 1 mRNA, complete

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RNLIPRNA 1534 bp mRNA linear ROD 19-FEB-1992
R.norvegicus mRNA for lipase.
X61925
X61925.1 GI:56599
lipase gene; triacylglycerol acyl hydrolase; triacylglycerol
lipase.
Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1534)
Wicker-Planquart,C. and Puigserver,A.
Primary structure of rat pancreatic lipase mRNA
FEBS Lett. 296 (1), 61-66 (1992)
92111786
LINE 1730292
2 (bases 1 to 1534)
Wicker-Planquart,C.
Direct Submission
LE Submitted (03-JUL-1991) C. Wicker-Planquart, CBM-CNRS, 31, Chemin
Joseph-Aiguier B.P.71, F-13402 Marseille Cedex 09, FRANCE
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polyA_signal 1510. .1515
polyA_site 1531
BASE COUNT 410 a 392 c 385 g 347 t
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QY 295 GATGCCAAATGGCAGAGAGACATGTGCAATGTGTGTCACAGCTGGAAGATATAAATTC 354
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QY 355 ATTAATTTAGATTGGATCAACAGTTTCAAGG---GAATACATCCATGCTGTAAACATCTC 411
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mat\_peptide

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polyA\_signal

polyA\_site

BASE COUNT 410 a 392 c 385 g 347 t

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Best Local Similarity 56.48; Pred. No. 4.1e-79;  
Matches 797; Conservative 0; Mismatches 598; Indels 18; Gaps 5;

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832	AACCATGCCGAAGTTATCAATTTTATGCTGAAGCATCTTAATCTCGATGCATTTATT	891
910	AACCACCTGGAAGCTACAAGTACTACTTTGGAGAGCATCCCTTAACCTGTATGGGTTCCGT	969
932	GCATTATCCTTTGATAGTCCACACATCTTTTAAAGCAGGAAATTGCTCTTTTGTTCAAA	951
970	GCATACCCCTGTGCTTCTCTACAGGACTTTGAGTCTAACAAATGCTCCCTCGCCAGAT	1029
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LT 14	AF1177402	2338 bp	linear	ROD 13-SEP-1999
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NITATION	lipase (PTL) mRNA, complete cds.			
SSION	AF1177402			
ION	AF1177402.1	GI:5762485		
OROS				
CE	Spermophilus tridecemlineatus	(thirteen-lined ground squirrel)		
GANISM	Spermophilus tridecemlineatus			
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	Sciurognathi; Sciuridae; Sciurinae;			
	Spermophilus.			
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THORS	Bauer, V.W. and Andrews, M.T.			
TLE	Direct Submission			
JURNAL	Submitted (13-AUG-1999) Genetics, North Carolina State University,			
	3513 Gardner Hall, Raleigh, NC 27695, USA			
RENCE	2 (bases 1 to 2338)			
THORS	Bauer, V.W. and Andrews, M.T.			
TLE	Direct Submission			
JURNAL	Submitted (13-SEP-1999) Genetics, North Carolina State University,			
	3513 Gardner Hall, Raleigh, NC 27695, USA			
MARK	Amino acid sequence updated by submitter			
URES	Location/Qualifiers			

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STON	mRNA, complete cds.	
ON	AF395870	
RDS	AF395870.1 GI:14701914	
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	Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;	
	Spermophilus.	
ENCE	1 (bases 1 to 1846)	
HORS	Squire, T.L., Bauer, V.W., Lowe, M.E. and Andrews, M.T.	
LE	Genomic Organization of the Pancreatic Triacylglycerol Lipase Gene	
	in a Hibernating Mammal	
TRNAL	Unpublished	
ENCE	2 (bases 1 to 1846)	

## AUTHORS

Squire, T.L. and Andrews, M.T.

## TITLE

Direct Submission

## JOURNAL

Submitted (28-JUN-2001) Department of Biology, University of Minnesota, Duluth, 10 University Drive, Duluth, MN 55812, USA

## FEATURES

Location/Qualifiers

## source

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## BASE COUNT

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## ORIGIN

## Query Match

24.5%; Score 344.2; DB 10; Length 1846;

## Best Local Similarity

57.1%; Pred. No. 8.3e-73;

## Matches

792; Conservative 0; Mismatches 568; Indels 27; Gaps 8;

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## Db

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time : 5234 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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US-10-038-517-1

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processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_esti:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estcom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_gsa1:\*

29: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	447.2	31.9	890	10 BF976776	BF976776 602146609
4	378	26.9	769	10 BG741031	BG741031 602634759

5	373.4	26.6	1528	11 AK028105	AK028105 Mus muscu
6	338.2	24.1	1513	11 BC007025	BC007025 Homo sapi
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8	318.8	22.7	1560	11 AK008021	AK008021 Mus muscu
9	300.6	21.4	757	13 BX259514	BX259514 BX259514
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11	282.4	20.1	795	13 EU417084	EU417084 603671129
12	277.6	19.8	761	13 EU416864	EU416864 603671085
13	274.8	19.6	780	13 EU416411	EU416411 603551210
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23	258.8	18.4	821	13 EU489555	EU489555 604128003
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EST.  
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1 (bases 1 to 892)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE  
Unpublished  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
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VERSION BC015840.1 GI:16198383
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1069)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NTH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgaps-help@mail.nih.gov
Tissue Procurement: ATCC/DCID/DTF
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbio.org
Anup Madan, Jessica Fahey, Erin Heiton, Mark Kettman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
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This clone has the following problem: retained intron.

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 1315 AATACATCTGGGAAATPATGATATATAAATCTACTCTTCTGTAGCAGACATTATGGACCT 1374  
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 mRNA sequence.

SIION  
 ON BP976776.1 GI:12343991

RDS  
 EST.

E Homo sapiens (human)

ANISM

ENCE  
 HORS  
 LE  
 RNAL  
 NT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: ARCC/DCTD/DTF  
 cDNA Library Preparation: CLONETECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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/clone="IMAGE:4305314"

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/clone\_lib="NIH MGC 62"

/notes="Organ: skin; Vector: pDNR-LIB (Clontech); Site\_1:  
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 Double-stranded cDNA was prepared from cell line RNA. 5'  
 and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-CAGCGCATTTAGCC-3' and 3' adaptor  
 sequence: 5'-ATTCTAGAGCGCGGCGGCGACATG-dT(30)BN-3'  
 (where B = A, C, G, or T). Average  
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 Laboratories (Palo Alto, CA)."

277 a 173 c 200 g 240 t

COUNT

IN

RES  
 source

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

NIH-MGC http://imgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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 DB 298 ACTTACACAAAATTAATCGATGCGAGTGTAACTGTTGAACATTACAAAGTGTTCAGTTC 357

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 BG741031  
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 mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

ORGANISM  
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 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

NIH-MGC http://imgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM10637 row: f column: 15  
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Location/Qualifiers

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277 a 173 c 200 g 240 t

COUNT

IN

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Average insert size 1.5kb. Library constructed by Life
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COUNT 240 a 134 c 164 g 231 t
IN

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Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
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related protein 1, full insert sequence.
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CE Mus musculus (house mouse)
GANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
THORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TLE High-efficiency full-length cDNA cloning
URNAL Meth. Enzymol. 303, 19-44 (1999)
DLNE 99279253
UBED 10349636
RENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
THORS Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
TLE Genome Res. 10 (10), 1617-1630 (2000)
URNAL 20499374
DLNE 11042159
UBED 3
RENCE 3
SHIBATA, K., ITOH, M., AIZAWA, K., NAGAKURA, S., SASAKI, N., CARNINCI, P.,
KONNO, H., AKIYAMA, J., NISHI, K., KITSUNAI, T., TASHIRO, H., ITOH, M.,

```

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Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
Genome Res. 10 (11), 1757-1771 (2000)
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4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
Aizawa, K., Okazaki, Y., Gojobori, T., Bono, H., Kondo, S., Yanagawa, T.,
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Kato, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bona, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Sessa, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1528)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numata, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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[illegible]

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REFERENCE	1 (bases 1 to 1513)
AUTHORS	Strausberg,R.

Direct Submission  
 Submitted (30-APR-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: CLONTECH  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
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 Db 1063 GGTATGCCAGTAATTTTGACGTTGGAGGTATAGGTATCTGTACATCTGTCTGGAAA 1122  
 QY 1099 GAAGTCTCAAGGAATCTTCTTCTTGTGTAGGCGGGCAATTTGGGAAAACCTGGGGAG 1158  
 Db 1123 AAGGTAC---AGGACACATAGTATTCTTTTCTTGGAAATAAGGAAACTCTAAGCAG 1179  
 QY 1159 TTTGCCATTTGCTAGTGGAAACCTTGAGCCAGGATGACTTTACACAAATTAATTCGATGA 1218  
 Db 1180 TATGAAATTTTCAAGGGCACTCTCAACACAGATGATCTCATTTCCATGAATTTGACTCA 1239  
 QY 1219 GATGTTAACGTTGGAACATTTACAAGTGTTCAGTTTCTGTTGTTGTTGTTGTTGTTGTTG 1278  
 Db 1240 GATGTGATGTTGGGGACTTGCAGATGGTTAAATTTTATTTGGTATTAACAATGTGATCAAC 1299  
 QY 1279 GATTTCTAGATAAGTTGGGAGCAGAAATGGTGTATAATATACATCTGGGAAATATGATAT 1338  
 Db 1300 CCAACTTTTACCTAGAGTGGAGCATCCAGATTTATAGTGGAGAC---AAATGTTGGAAA 1356  
 QY 1339 AAATCTACCTTCTCTAGCCAGACATTTATGGGACCTTAATTTCTCCAGAACCTTGAACCA 1398  
 Db 1357 CAGTTCACTTCTGTATCCAGAAACCGTCCAGGAGGAGGAGTTCTGTCTACCTCCACACCG 1416  
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 Db 1417 TGTTA 1421

RESULT 7  
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 LOCUS 601854965P1 NIH\_MGC\_57 Homo sapiens cDNA clone IMAGE:4074544 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF246347  
 VERSION BF246347.1 GI:11160614

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JDS
DE Homo sapiens (human)
JANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 682)
RNC NH-MGC http://mgc.nci.nih.gov/.
RHS National Institutes of Health, Mammalian Gene Collection (MGC)
FILE Unpublished
JRNAL Contact: Robert Strausberg, Ph.D.
ENT Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM925 row: b column: 17
High quality sequence stop: 552.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4074544"
/tissue_type="glioblastoma"
/lab_host="PH10B (T1 phage-resistant)"
/clone_lib="NH_MGC_57"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggcgctggccg); Site 2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCAGACCGCCGCGCATG-3' and 3' adaptor
sequence: 5'-ATTCAGACCGCCGCGCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
COUNT 206 a 130 c 155 g 190 t 1 others
IN
ery Match 23.5%; Score 329.8; DB 10; Length 682;
st Local Similarity 95.8%; Pred. No. 2.2e-77;
:ches 392; Conservative 0; Mismatches 12; Indels 5; Gaps 5;
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1 ATATGACAGCTAATGATCACAATTATTTTAAACACAGGGTCCCTTCCCATTTGCC 60
1060 GTTGGAGGACAAATGTCTGTTAACTCAGTGGAGCGAAGTCACTCAAGAACTGTC 1119
61 GTGGAGGACAAATGTCTGTTAACTCAGTGGAGCGAAGTCACTCAAGAACTGTC 120
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121 TTTCTTCGTAGCGGGGCAATGTGGAAAACTGGGGAGTTTGCCATTTGTCAAGTGA 180
1178 AACTTGAGCAGCGATGCTTACACAAATTAATCGATGCAGATGTTACGTTGGAACA 1237
181 AACTTGAGCAGCGATGCTTACACAAATTAATCGATGCAGATGTTACGTTGGAACA 240
1238 TTACAAGTGTTCAGTTTCATCTCGSAAAAACATTTGTTTGAAGATTCAGAAATAGTTGG 1297
241 TTACAAGTGTTCAGTTTCATCTCGSAAAAACATTTGTTTGAAGATTCAGAAATAGTTGG 300
1298 GAGCAGAAAT-GGTGATAATACATCT-GGGAATATGGATATAAATCTACCTCTGTG 1355
301 GAGCAGAAATGGGTGATAATACATCTGGGGAATATGGATATAAATCTACCTCTGTG 360
1356 CCAAGACATTATGGGACCTAATTAATCTCCAGAACCTGAAACCATGCTAA 1404

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361 CCAGACATTATGGACCTTAATATCTCCAGAACCTGGAAACCATCTTA 409

DB

RESULT 8  
AK008021  
LOCUS  
DEFINITION

Mus musculus adult male small intestine cDNA, RIKEN full-length  
enriched library, clone:2010001015 product:pancreatic  
lipase-related protein 2, full insert sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AK008021 1560 bp mRNA linear HTC 05-DEC-2002  
AK008021  
Mus musculus adult male small intestine cDNA, RIKEN full-length  
enriched library, clone:2010001015 product:pancreatic  
lipase-related protein 2, full insert sequence.  
AK008021  
AK008021.1 GI:12841949  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
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High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349836

2  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and analysis of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
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20499374  
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Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
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Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
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sequencing pipeline with 384 multicapillary sequencer  
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20530913  
11076861

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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,  
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,  
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,  
Saito,T., Okazaki,Y., Gotohori,T., Bono,H., Kasukawa,T., Saito,R.,  
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,  
Fleischmann,W., Gaasterland,T., Glessi,C., King,B., Kochiwa,H.,  
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,  
Quackenbush,J., Schriml,L.M., Stauble,F., Suzuki,R., Tomita,M.,  
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,  
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Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,  
Fletcher,C., Fujita,M., Cariboldi,M., Gustincich,S., Hill,D.,  
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,  
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,  
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21085660  
11217851

5  
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Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED

6 (bases 1 to 1560)

RENCHE  
THORS

Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,  
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,  
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,  
Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,  
Kasukawa,T., Kato,H., Kawajiri,J., Kojima,Y., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Masuyama,T., Miyazaki,A., Nishi,K., Oda,  
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,  
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,  
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,  
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,  
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,  
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TLE  
URNAL

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216).

ENT

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
[5'-GAGAGAGAGATCCAGAGCTTTTTCCTTTTTTTN 3'], cDNA was  
prepared by using triazole thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. cDNA went  
through one round of normalization to Rot = 5.0 and subtraction to  
Rot = 20.0. Second strand cDNA was prepared with the primer adapter  
of sequence [5'-  
GAGAGAGATTCGAGTTAATAATTAAATCCCCCCCCCCC 3']. cDNA was cleaved  
with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.  
Host: SOLR.

URES

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misc\_feature

polyA\_signal

polyA\_site

COUNT 405 a 398 c 391 g 366 t

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 1343 CTACCTTCTGACCAAGACATTTATGGGACCTTAATATCTCCAGAACCTGAAACCATGCT 1402  
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 1403 AA 1404  
 1517 AA 1518

IT 9  
 514

ITITION BX259514 757 bp mRNA linear EST 27-FEB-2003  
 BX259514 AGENAE Gallus multi-tissues normalized library  
 (gcag) Gallus gallus cdna clone gcag0007c.o.07 5prim, mRNA  
 sequence.

STON BX259514 1 GI:28582112  
 ON BX259514  
 RDS EST.

ANISM Gallus gallus (chicken)

Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus;

1 (bases 1 to 757)  
 Herault, F., Le Muth-Metzinger, V., Desert, C., Retout, E., Piumi, F.,  
 Klopp, C. and Douaire, M.

Construction and primary characterization of chicken normalized  
 multi-tissue cDNA libraries  
 Unpublished

Contact: Douaire M  
 INRA, UMR INRA-ENSAR Genetique Animale  
 65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE  
 Tel.: +33 (0) 2.23.48.54.63

Fax: +33 (0) 2.23.48.54.70

Email: Madeleine.Douaire@roazhon.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us  
 at signasupport@jouy.inra.fr to obtain the chromatogram of this  
 sequence.

Plate: 0007 row: 0 column: 7

Seq primer: M13R.

RES  
 source

Location/Qualifiers  
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 adipose tissue, granulosa, utero-vaginal gland, oviduct,  
 small follicle, ovary, hypothalamus, pituitary gland,  
 ileon, jejunum, caecum, duodenum, spleen, fabricius gland  
 , bone marrow, thymus, hematopoietic progenitor cells.  
 Clone distribution : AGENAE Resource centre. Francois  
 PIUMI, Francois, Piumi.inra.fr, INRA, CEA Radiobiologie et  
 Etude du genome (LREG), Domaine de Vilvert, 78352,  
 Jouy-en-Josas cedex, FRANCE"

COUNT 223 a 156 c 191 g 186 t 1 others

ry Match

21.4%; Score 300.6; DB 13; Length 757;

Best Local Similarity 64.6%; Pred. No. 1.7e-69;  
 Matches 482; Conservative 0; Mismatches 255; Indels 9; Gaps 2;

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QY	82	TTCAAAGATGGTTTACCATGGACAGGACTTTTCTCAACAGAGTTGGTAGTTTACCCTTGG	141
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QY	142	TCTCCAGAGAGATAAACATCTGTTTCTGCTCTACACTATACACATCCCAATGCCCTAT	201
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QY	316	ATGTGCAATGTTGCTACAGCTGGAAGATATAAATTCATTAAATTTAGATTGATCAAC	375
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QY	376	GGTTCACGG---GAATACATCATGCTCTTAACAAATCTCCGTGTTGTTGGTGTGAGGTG	432
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QY	433	GCTTATTTTATTGATGTTCTCATGAAAAAATTTGAATATCCCTTCTTAAAGTGCACCTTG	492
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QY	613	AGGTAGACCCCTCGGATGCCAACCTTTTGTGACGTTATTCATAAATGACAGCTCGCATC	672
Db	610	AGGTGCGATAAAGCGATGCAAGGTTTGTGATGTTATCCACACAGATACAGCTCCCAT	669
QY	673	CTCTTTGAGCTTGGTTGGAAACCATGATGCTTGTGTCATCTTGTATTTTACCCAAAT	732
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QY	733	GGAGGGAAGCACATGCCAGGATGTGA	758
Db	730	GGAGGAGTGGAAATGCCANGATGTGA	755

RESULT 10  
 BU416727

LOCUS BU416727

DEFINITION

603671286F1 CSEQEBL07 Gallus gallus cdna clone CHES1615121 5', mRNA

sequence.

ACCESSION BU416727

VERSION BU416727.1

GI:25909398

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 778)

Boardman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,

Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.

A Comprehensive Collection of Chicken cDNAs

REFERENCE

AUTHORS

TITLE

URNAL  
LINE  
URNED  
ENT

Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)

PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

URES  
source

Location/Qualifiers  
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Site 1: EcoRI; Site 2: NotI; Modification of pBluescript  
II KS(+) [Stratagene] vector to accommodate cDNA produced  
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uni-directionally cloned cDNA libraries from messenger RNA  
for improved 3' end DNA sequencing by Glenn Fu, et al.  
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with  
NotI and EcoRI. Ligate in double stranded adaptor  
containing BspI and BamHI sites  
[5'ggccgcgtgcagcccgatccgaaaaaag]  
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159 c 194 g 191 t 1 others

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QY CATCTTGACITTTTACCCCAATGGAGGAGCACATCCAGGATGGA 758  
Db CATCTTGACITTTTATCCAAACGGAGGAGTGGAAATCCAGGATGGA 769

RESULT 11  
BU417084

LOCUS BU417084 795 bp mRNA linear EST 29-NOV-2002  
DEFINITION 603671179F1 CSQRBL07 Gallus gallus cDNA clone CHEST615n20 5', MENA  
sequence.

ACCESSION BU417084

VERSION BU417084.1 GI:25909755

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM

Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 795)  
Fong, W.T., Tickle, C., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392

COMMENT

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Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. .795

source

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Layer and broiler"

/db\_xref="taxon:9031"

/clone="CHEST615n20"

/sex="Male and female"

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/note="Organ: pancreas; Vector: pBluescript II KS(+);  
Site 1: EcoRI; Site 2: NotI; Modification of pBluescript  
II KS(+) [Stratagene] vector to accommodate cDNA produced  
with the T-trimmed protocol (Construction of  
uni-directionally cloned cDNA libraries from messenger RNA  
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U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with  
NotI and EcoRI. Ligate in double stranded adaptor  
containing BspI and BamHI sites  
[5'ggccgcgtgcagcccgatccgaaaaaag]  
[5'aattcttttttcggatccgggtgcagc]"  
159 c 194 g 191 t 1 others

BASE COUNT 236 a 161 c 200 g 198 t  
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Query Match 20.1%; Score 282.4; DB 13; Length 795;  
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 ches 487; Conservative 0; Mismatches 256; Indels 11; Gaps 4;

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 761)  
 ENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 HORS Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22355534  
 PUBMED 12445392  
 COMMENT

CONTACT: Simon Hubbard  
 Department of Biomolecular Sciences  
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 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
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 Site 1: EcoRI; Site 2: NotI; Modification of pBluescript  
 II KS(+) [Stratagene] vector to accommodate cDNA produced  
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 U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with  
 NotI and EcoRI. Ligate in double stranded adaptor  
 containing BspI and BamHI sites  
 [5'ggcgcgtgcagccgcggtccggaagaaag]  
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 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
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/organism="Gallus gallus"  
 /mol\_type="mRNA"  
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 VERSION  
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 ORGANISM  
 Gallus gallus  
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 Phasianinae; Gallus.  
 1 (bases 1 to 741)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
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 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
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 /organism="Gallus gallus"  
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 /note="Organ: pancreas; Vector: pBluescript II KS(+);  
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 [5'ggccgctgcagcccgatccgagaaag  
 [5'aattcttttcgagtcggcgctgcagc]"  
 217 a 154 c 183 g 187 t

FEATURES  
 source

BASE COUNT

IN

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tches 474; Conservative 0; Mismatches 252; Indels 11; Gaps 4;

1 ATGCTTGGAATTTGGATTGTTGCAATCTTCTTTGGCCACATCAAGAGGAAAGAAAGTT 60  
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7 ATGCTTCGAATTTGGGATATTCGCGCTATTTCTCTCGCACAGCGCTCTGAAGTT 66  
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time : 3198 secs